

Table 2B

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SEQ ID	Hit ID	Species	Description	S score	% Identity
1697	AAE22224	Homo sapiens	Human 5685C6 protein.	542	98
1697	ABG40551	Homo sapiens	Human peptide encoded by genome-derived single exon probe SEQ ID 30216.	516	98
1697	AAM18652	Homo sapiens	Peptide #5086 encoded by probe for measuring cervical gene expression.	516	98
1698	AAM39274	Homo sapiens	Human polypeptide SEQ ID NO 2419.	1596	79
1698	AAB29653	Homo sapiens	Human membrane-associated protein HUMAP-10.	1596	79
1698	gi9858855	Homo sapiens	HPT protein	1596	79
1699	gi6841138	Homo sapiens	HSPC099	275	100
1699	AAB93037	Homo sapiens	Human protein sequence SEQ ID NO:11816.	130	23
1699	AAB61308	Homo sapiens	Human transcriptional regulator protein #8.	125	22
1700	AAM93959	Homo sapiens	Human polypeptide, SEQ ID NO: 4164.	1182	99
1700	AAB36587	Homo sapiens	Human FLEXHT-9 protein sequence SEQ ID NO:9.	590	53
1700	AAB93652	Homo sapiens	Human protein sequence SEQ ID NO:13161.	586	54
1701	gi30264	Homo sapiens	cystatin D	392	100
1701	gi16116526	Homo sapiens	yX60D10.1 (cystatin D)	387	100
1701	AAO15149	Homo sapiens	Human cystatin D protein sequence.	380	98
1702	gi1374754	Staphylothermus marinus	tetrabrachion	72	27
1703	AAE17127	Homo sapiens	Human GnT-V protein.	628	77
1703	AAB48911	Homo sapiens	Human beta-1,6-N-acetylglucosamine transferase (GnT-V).	628	77
1703	AAB83010	Homo sapiens	Human GnT-V.	628	77
1704	AAV68736	Homo sapiens	Short chain alcohol dehydrogenase-related molecule ScRM-2 cDNA.	1249	81
1704	AAV69295	Homo sapiens	A human human protein, designated HSPC021 (CBFAIG06).	1249	81
1704	AAB58463	Homo sapiens	Lung cancer associated polypeptide sequence SEQ ID 801.	1249	81
1705	gi15294065	Ictalurus punctatus	40S ribosomal protein S26-2	212	58
1705	ABP42978	Homo sapiens	Human ovarian antigen HPDWD69, SEQ ID NO:4110.	208	58
1705	AAG76127	Homo sapiens	Human colon cancer antigen protein SEQ ID NO:6891.	208	58
1706	gi6580428	Homo sapiens	IkappaBR	2759	95
1706	gi14250636	Homo sapiens	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2	2606	86
1706	gi746415	Homo sapiens	I kappa BR	1655	71
1707	AAM79219	Homo sapiens	Human protein SEQ ID NO 1881.	325	64
1708	gi5901529	Homo sapiens	C2H2 type Kruppel-like zinc finger protein splice variant b	565	99
1708	gi5901527	Homo sapiens	C2H2 type Kruppel-like zinc finger protein	317	33
1708	gi15029916	Mus musculus	Similar to Zinc finger protein 118	296	31

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SEQ ID	Hit ID	Species	Description	S score	% Identity
1709	AAU85415	Homo sapiens	Human protein NOV13.	953	98
1709	AAU72895	Homo sapiens	Human metalloprotease partial protein sequence #7.	925	100
1709	AAU74750	Homo sapiens	Human protease PRTS-10 protein sequence.	925	100
1710	gi12862392	Mus musculus	D86	2863	64
1710	ABG37531	Homo sapiens	Human peptide encoded by genome-derived single exon probe SEQ ID 27196.	1687	100
1710	AAM03553	Homo sapiens	Peptide #2235 encoded by probe for measuring breast gene expression.	1687	100
1711	gi1787337	acyl-carrier-protein synthase II [Escherichia coli K12]	3-oxoacyl-	315	91
1711	gi12514639	acyl-carrier-protein synthase II [Escherichia coli O157:H7 EDL933]	3-oxoacyl-	315	91
1711	gi664870	Escherichia coli	beta-ketoacyl-acyl carrier protein synthase II	315	91
1712	AAG75407	Homo sapiens	Human colon cancer antigen protein SEQ ID NO:6171.	1258	82
1712	AAR89952	Homo sapiens	Insulin-like growth factor binding protein-3.	1232	80
1712	AAU85512	Homo sapiens	Clone #19095 (L549S) of lung tumour protein.	1228	80
1713	AAB94696	Homo sapiens	Human protein sequence SEQ ID NO:15673.	710	97
1713	AAB99892	Homo sapiens	Human RNA helicase gene helicain C protein sequence SEQ ID NO:6.	710	97
1713	AAB99891	Homo sapiens	Human RNA helicase gene helicain B protein sequence SEQ ID NO:4.	710	97
1714	gi15384740	Homo sapiens	paralemm-2	1652	100
1714	gi15384742	Homo sapiens	Palm2-AKAP2 fusion protein	1577	100
1714	gi14041780	Homo sapiens	AKAP-2 protein	410	73
1715	gi13021825	Homo sapiens	polymerase	575	48
1715	gi3600067	Homo sapiens	polymerase	572	48
1715	gi1780973	Human endogenous retrovirus K	pol protein	572	48
1717	gi35825	Homo sapiens	pregnancy zone protein	6592	88
1717	gi579594	Homo sapiens	alpha 2-macroglobulin 690-740	4985	66
1717	AAR11749	Homo sapiens	Human alpha-2 macroglobulin bait region mutant.	4976	66
1718	gi13366277	Homo sapiens	dJ998H6.1 (ortholog of rat PB-Cadherin)	1167	93
1718	gi4760578	Mus musculus	PB-Cadherin	1028	84
1718	gi1398912	Rattus norvegicus	short type PB-cadherin	1022	84
1720	AAE06588	Homo sapiens	Human protein having hydrophobic domain, HP10778.	687	100
1720	AAM40979	Homo sapiens	Human polypeptide SEQ ID NO 5910.	687	100

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SEQ ID	Hit ID	Species	Description	S score	% Identity
1720	gi15072402	Raja erinacea	organic solute transporter alpha	357	45
1721	AAG81345	Homo sapiens	Human AFP protein sequence SEQ ID NO:208.	839	62
1721	gi16359082	Homo sapiens	Similar to RIKEN cDNA 2810049G06 gene	839	62
1721	AAB93797	Homo sapiens	Human protein sequence SEQ ID NO:13560.	836	62
1722	gi871883	Homo sapiens	lanosterol 14-demethylase	2180	99
1722	gi1809225	Homo sapiens	lanosterol 14-demethylase (cytochrome p450)	2180	99
1722	gi1698396	Homo sapiens	lanosterol 14-demethylase cytochrome P450	2180	99
1723	ABG41541	Homo sapiens	Human peptide encoded by genome-derived single exon probe SEQ ID 31206.	232	100
1723	AAM32019	Homo sapiens	Peptide #6056 encoded by probe for measuring placental gene expression.	232	100
1723	AAM71727	Homo sapiens	Human bone marrow expressed probe encoded protein SEQ ID NO: 32033.	232	100
1724	AAV53040	Homo sapiens	Human secreted protein clone kj320_1 protein sequence SEQ ID NO:86.	2480	100
1724	gi3510639	Rattus norvegicus	UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5	1345	59
1724	gi6688167	Homo sapiens	GalNAc-T5	1082	100
1725	ABP41917	Homo sapiens	Human ovarian antigen H6EDF71, SEQ ID NO:3049.	1329	97
1725	AAG75406	Homo sapiens	Human colon cancer antigen protein SEQ ID NO:6170.	1329	97
1725	gi396176	Homo sapiens	antigenic surface determinant OA3	1329	97
1726	AAU79036	Homo sapiens	Human SHPS-1 (not defined) receptor.	858	98
1726	AAW40481	Homo sapiens	Human SH2 binding protein.	858	98
1726	AAW49909	Homo sapiens	Signal regulatory protein 4 (SIRP4).	858	98
1727	gi2707601	Homo sapiens	synaptophysin	1656	100
1727	gi15928723	Mus musculus	synaptophysin	1585	94
1727	gi57326	Rattus norvegicus	synaptophysin (AA 1-307)	1577	95
1728	gi15590682	Homo sapiens	histone deacetylase 9a	628	96
1728	gi15590680	Homo sapiens	histone deacetylase 9	628	96
1728	gi12060992	Mus musculus	MEF2-interacting transcription repressor MITR	625	95
1729	gi21430596	Drosophila melanogaster	RE16431p	891	39
1729	gi14164377	Mus musculus	Type II membrane protein of ER~mouse gene similar to alpha-mannosidase	350	33
1729	gi1504008	Homo sapiens	Containing ATP/GTP-binding site motif A(P-loop): Similar to C.elegans protein(P1:CEC47E128);Similar to Mouse alpha-mannosidase(P1:B54407)	346	33
1730	gi7861753	Mus musculus	GABA-A receptor epsilon-like	412	32

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SEQ ID	Hit ID	Species	Description	S score	% Identity
			subunit		
1730	gi11610622	Rattus norvegicus	GABA-A epsilon subunit splice variant	411	32
1730	gi7861743	Rattus norvegicus	GABA-A receptor epsilon-like subunit	411	32
1731	AAW80135	Homo sapiens	Human recombinant neurokinin-2 (NK-2) receptor protein.	1743	95
1731	gi189222	Homo sapiens	neurokinin-2 receptor	1743	95
1731	gi189135	Homo sapiens	neurokinin A receptor	1742	95
1732	AAB75594	Homo sapiens	Human secreted protein sequence encoded by gene 37 SEQ ID NO:148.	678	99
1732	AAB80437	Homo sapiens	Gene #20 associated peptide #1.	381	98
1732	AAM78175	Homo sapiens	Human bone marrow expressed probe encoded protein SEQ ID NO: 38481.	365	100
1733	ABB84853	Homo sapiens	Human PRO1120 protein sequence SEQ ID NO:74.	293	100
1733	ABB90378	Homo sapiens	Human polypeptide SEQ ID NO 2754.	293	100
1733	ABB95459	Homo sapiens	Human angiogenesis related protein PRO1120 SEQ ID NO: 74.	293	100
1734	ABB07527	Homo sapiens	Human drug metabolizing enzyme (DME) (ID: 5643401CD1).	1652	79
1734	ABB07515	Homo sapiens	Human drug metabolizing enzyme (DME) (ID: 8097779CD1).	867	73
1734	gi13161409	Mus musculus	family 4 cytochrome P450	718	58
1735	AAM40183	Homo sapiens	Human polypeptide SEQ ID NO 3328.	1322	67
1735	AAY71159	Homo sapiens	Human phosphodiesterase interacting protein, myomegalin.	1322	67
1735	gi4761644	Rattus norvegicus	myomegalin	886	44
1736	AAM94312	Homo sapiens	Human reproductive system related antigen SEQ ID NO: 2970.	500	71
1736	ABJ03726	Homo sapiens	Human ovary specific protein SEQ ID NO: 168.	298	41
1736	gi8439396	HERV-H/env62	envelope protein	292	40
1737	AAY76177	Homo sapiens	Human secreted protein encoded by gene 54.	288	100
1738	AAY92075	Homo sapiens	Human DKR-4.	759	100
1738	AAB08875	Homo sapiens	Amino acid sequence of a human Dickkopf (Dkk)-4 protein.	759	100
1738	AAW73017	Homo sapiens	Human cysteine-rich secreted protein CRSP-2.	759	100
1739	ABB97828	Homo sapiens	Human secretory polypeptide (SPTM) 80.	2007	86
1739	ABB90159	Homo sapiens	Human polypeptide SEQ ID NO 2535.	1547	98
1739	gi18642980	Homo sapiens	GTPase	1524	61
1740	AAB49278	Homo sapiens	Protein encoded by zsig81 cDNA fragment.	755	94
1740	AAU29276	Homo sapiens	Human PRO polypeptide sequence #253.	755	94
1740	gi12003127	Eremothecium	GTPase activating protein BEM2	83	28

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SEQ ID	Hit ID	Species	Description	S score	% Identity
		<i>gossypii</i>			
1741	gi21707232	Homo sapiens	similar to choline transporter-like protein	1637	76
1741	AAB65196	Homo sapiens	Human PRO1115 (UNQ558) protein sequence SEQ ID NO:177.	1636	76
1741	AAB87541	Homo sapiens	Human PRO1115.	1636	76
1742	AAG66142	Homo sapiens	Human PAS Kinase (PASK) polypeptide.	2227	99
1742	AAM79231	Homo sapiens	Human protein SEQ ID NO 1893.	2227	99
1742	AAM79230	Homo sapiens	Human protein SEQ ID NO 1892.	2227	99
1743	gi13879899	Mycobacterium tuberculosis CDC1551	PPE family protein	102	27
1743	gi2653311	Bovine herpesvirus type 1.1	very large virion protein (tegument)	99	27
1743	gi1491621	Bovine herpesvirus 1	UL36	99	27
1744	gi5931718	Chlamydomonas reinhardtii	1-alpha dynein heavy chain	2126	56
1744	gi9409781	Chlamydomonas reinhardtii	1 beta dynein heavy chain	1121	34
1744	gi514215	Chlamydomonas reinhardtii	dynein beta heavy chain	1070	33
1745	AAB53088	Homo sapiens	Human angiogenesis-associated protein PRO328, SEQ ID NO:132.	1972	89
1745	AAB80260	Homo sapiens	Human PRO328 protein.	1972	89
1745	AAU12351	Homo sapiens	Human PRO328 polypeptide sequence.	1972	89
1746	AAU29172	Homo sapiens	Human PRO polypeptide sequence #149.	730	68
1746	AAY99398	Homo sapiens	Human PRO1301 (UNQ667) amino acid sequence SEQ ID NO:212.	730	68
1746	AAM38651	Homo sapiens	Human polypeptide SEQ ID NO 1796.	728	68
1747	AAE21056	Homo sapiens	Human drug metabolising enzyme (DME-14) protein.	111	59
1748	AAE03560	Homo sapiens	Human differentially expressed kidney cDNA 22360 encoded protein.	1140	88
1748	AAM42434	Homo sapiens	Human kidney related polypeptide SEQ ID NO 303.	466	98
1748	AAM99619	Homo sapiens	Human excretory related polypeptide SEQ ID NO 356.	466	98
1749	AAE22911	Homo sapiens	Human transporter and ion channel (TRICH) 10.	2309	100
1749	gi13506805	Homo sapiens	thymic stromal co-transporter	2309	100
1749	gi13506808	Mus musculus	thymic stromal co-transporter	1782	77
1750	gi18157547	Mus musculus	pecanex-like 3	7005	89
1750	gi15076843	Homo sapiens	pecanex-like protein 1	4359	51
1750	gi13171105	Takifugu rubripes	pecanex	4118	58
1751	AAY06603	Homo sapiens	Retinoblastoma interacting protein GluT1*.	411	100
1751	gi825504	Homo sapiens	glutamate transporter	411	100

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SEQ ID	Hit ID	Species	Description	S score	% Identity
1751	gi825663	Homo sapiens	GLAST1	411	100
1752	gi2078518	Homo sapiens	neogenin	593	100
1752	gi641966	Gallus gallus	neogenin	591	98
1752	gi1785999	Rattus norvegicus	neogenin	586	97
1753	ABB53278	Homo sapiens	Human polypeptide #18.	315	26
1753	ABB53277	Homo sapiens	Human polypeptide #17.	315	26
1753	AAP94014	Homo sapiens	Carcinoembryonic cell surface antigen.	225	25
1754	AAO21681	Homo sapiens	Human secreted protein SEQ ID No 23.	443	95
1754	AAB75375	Homo sapiens	Human secreted protein #34.	443	95
1754	AAB88603	Homo sapiens	Human hydrophobic domain containing protein clone HP10770 #127.	443	95
1755	AAE22906	Homo sapiens	Human transporter and ion channel (TRICH) 5.	1973	90
1755	AAE16350	Homo sapiens	Human tetracycline transporter like-like protein, POLY14.	1969	90
1755	gi2506078	Mus musculus	tetracycline transporter-like protein	1961	90
1756	AAB88469	Homo sapiens	Human membrane or secretory protein clone PSEC0027.	1065	98
1756	AAE06608	Homo sapiens	Human protein having hydrophobic domain, HP10798.	1065	98
1756	AAM40347	Homo sapiens	Human polypeptide SEQ ID NO 3492.	1065	98
1757	gi8925284	Homo sapiens	phosphatidylinositol polyphosphate 5-phosphatase type IV	2599	91
1757	gi9295353	Mus musculus	inositol polyphosphate 5-phosphatase	1989	78
1757	gi5360761	Rattus norvegicus	pharbin	1928	77
1758	gi395207	Bos taurus	potassium channel (BGK5)	753	82
1758	gi186669	Homo sapiens	potassium channel	750	82
1758	gi304652	Canis familiaris	delayed rectifier K ⁺ channel	746	81
1759	AAB65058	Homo sapiens	Gene #7 associated peptide #12.	908	93
1759	AAB64999	Homo sapiens	Human secreted protein #7.	908	93
1759	AAU01099	Homo sapiens	Gene 35 Human secreted protein homologous amino acid sequence.	814	91
1760	AAU11384	Homo sapiens	Human T2R61 (hT2R61) polypeptide.	802	100
1760	gi20336531	Homo sapiens	candidate taste receptor T2RP1	794	99
1760	ABB06836	Homo sapiens	Human nGPCR-Seq1048 protein sequence SEQ ID NO:105.	718	79
1761	AAAY36115	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 500.	514	87
1761	AAW64556	Homo sapiens	Human osteocarcinoma cell line U-2 OS clone HP10305 protein.	514	87
1761	gi14250122	Homo sapiens	uncharacterized hematopoietic stem/progenitor cells protein MDS029	514	87
1762	AAG78575	Homo sapiens	Human SLC5A3 amino acid sequence.	3621	100
1762	AAB47976	Homo sapiens	BCW2.	3621	100
1762	gi2739094	Homo sapiens	sodium/myo-inositol cotransporter	3621	100
1763	ABB80578	Homo sapiens	Human sbg618069LRR protein #2.	3076	99

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SEQ ID	Hit ID	Species	Description	S score	% Identity
1763	ABB80577	Homo sapiens	Human sbg618069LRR protein #1.	1572	95
1763	AAW84596	Homo sapiens	Amino acid sequence of the human Tango-79 protein.	1209	44
1764	ABB81460	Homo sapiens	Human aggrecanase MDT58 protein SEQ ID NO:2.	3392	89
1764	gi19171150	Homo sapiens	ADAMTS18 protein	3364	89
1764	AAU72893	Homo sapiens	Human metalloprotease partial protein sequence #5.	2762	90
1765	gi1695682	Homo sapiens	hepatic triglyceride lipase	152	64
1765	gi32498	Homo sapiens	precursor (AA -23 to 476)	152	64
1765	gi339593	Homo sapiens	triglyceride lipase	152	64
1766	AAM79459	Homo sapiens	Human protein SEQ ID NO 3105.	1493	100
1766	AAM78475	Homo sapiens	Human protein SEQ ID NO 1137.	1493	100
1766	ABB11930	Homo sapiens	Human secreted protein homologue, SEQ ID NO:2300.	1493	100
1767	AAM47914	Homo sapiens	Human lysophosphatidic aminoacyl transferase 42.	324	90
1767	AAE15296	Homo sapiens	Human LPAAT delta protein.	324	90
1767	AAB65188	Homo sapiens	Human PRO1016 (UNQ499) protein sequence SEQ ID NO:156.	324	90
1768	AAE23757	Homo sapiens	Human metabotropic glutamate (mGluR4) receptor protein.	926	99
1768	AAR82658	Homo sapiens	Human mGluR4.	926	99
1768	gi1160183	Homo sapiens	metabotropic glutamate receptor type 4	926	99
1769	AAM41363	Homo sapiens	Human polypeptide SEQ ID NO 6294.	2370	98
1769	AAE17500	Homo sapiens	Human secretion and trafficking protein-9 (SAT-9).	2207	99
1769	AAM39577	Homo sapiens	Human polypeptide SEQ ID NO 2722.	2207	99
1770	AAB73512	Homo sapiens	Human transferase HTFS-19, SEQ ID NO:19.	264	45
1770	AAB56487	Homo sapiens	Human prostate cancer antigen protein sequence SEQ ID NO:1065.	264	45
1770	gi14249942	Homo sapiens	Similar to RIKEN cDNA 0610008P16 gene	264	45
1771	gi7678873	Homo sapiens	vascular cadherin-2	5369	99
1771	gi7407150	Homo sapiens	protocadherin 12	5369	99
1771	gi8164037	Homo sapiens	vascular endothelial cadherin 2	5369	99
1772	AAM93947	Homo sapiens	Human polypeptide, SEQ ID NO: 4138.	231	93
1772	AAM93886	Homo sapiens	Human polypeptide, SEQ ID NO: 4013.	231	93
1772	AAM93857	Homo sapiens	Human polypeptide, SEQ ID NO: 3949.	231	93
1773	gi1335205	Homo sapiens	ORFII	270	48
1773	AAB94891	Homo sapiens	Human protein sequence SEQ ID NO:16231.	263	62
1773	AAG73650	Homo sapiens	Human colon cancer antigen protein SEQ ID NO:4414.	263	58
1774	AAB93885	Homo sapiens	Human protein sequence SEQ ID NO:13815.	1088	85
1774	AAM93980	Homo sapiens	Human stomach cancer expressed polypeptide SEQ ID NO 29.	1088	85

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SEQ ID	Hit ID	Species	Description	S score	% Identity
1774	gi3603459	Homo sapiens	tetraspan NET-5	1088	85
1775	ABB06607	Homo sapiens	G protein-coupled receptor GPCR5 protein SEQ ID NO:24.	982	77
1775	AAG71597	Homo sapiens	Human olfactory receptor polypeptide, SEQ ID NO: 1278.	982	77
1775	gi21928553	Homo sapiens	seven transmembrane helix receptor	982	77
1776	AAB64888	Homo sapiens	Human secreted protein sequence encoded by gene 7 SEQ ID NO:66.	252	85
1776	AAB38011	Homo sapiens	Human secreted protein encoded by gene 3 clone HPJCX13.	252	85
1776	AAB94917	Homo sapiens	Human protein sequence SEQ ID NO:16357.	191	62
1777	gi182851	Homo sapiens	GOS2 protein	497	100
1777	gi1213013	Mus musculus	GOS2-like protein	377	77
1777	AAM79519	Homo sapiens	Human protein SEQ ID NO 3165.	81	26
1778	ABB89432	Homo sapiens	Human polypeptide SEQ ID NO 1808.	473	100
1778	ABP61790	Homo sapiens	Human polypeptide SEQ ID NO 144.	473	100
1778	AAV80991	Homo sapiens	Human VAMP-2 homologue, CBCBMH06.	473	100
1779	gi5264503	Mus musculus	sif and Tiam1-like exchange factor	82	30
1779	gi9295309	frog adenovirus 1	pIIa protein	78	40
1779	gi16415263	Listeria innocua	similar to two-component sensor histidine kinase	78	27
1780	gi21693020	Homo sapiens	MHC class I antigen	1311	70
1780	gi1399321	Macaca mulatta	MHC class I antigen Mamu B*08	1307	71
1780	gi8117799	Pan troglodytes	MHC class I antigen	1302	70
1781	ABB75677	Homo sapiens	Breast protein-eukaryotic conserved gene 1 (BSTP-ECG1) protein.	754	40
1781	AAU29191	Homo sapiens	Human PRO polypeptide sequence #168.	754	40
1781	AAV99421	Homo sapiens	Human PRO1433 (UNQ738) amino acid sequence SEQ ID NO:292.	754	40
1782	gi2343157	Homo sapiens	peroxisomal membrane protein 69	2796	89
1782	gi2706518	Homo sapiens	peroxisomal ABC-transporter	2796	89
1782	gi15215442	Homo sapiens	Similar to ATP-binding cassette, sub-family D (ALD), member 4	2788	88
1783	AAB35235	Homo sapiens	Human neurotransmitter transporter protein GC42.	3573	98
1783	AAB35236	Homo sapiens	Human glycine transporter type 1c.	3559	98
1783	gi546769	Homo sapiens	glycine transporter type 1b; GlyT-1b	3559	98
1784	AAU00017	Homo sapiens	Human Plexin-D1.	7512	90
1784	ABB11709	Homo sapiens	Human plexin-B1/SEP receptor homologue, SEQ ID NO:2079.	7467	90
1784	gi5918167	Homo sapiens	plexin-B1/SEP receptor	2120	33
1785	ABB44591	Homo sapiens	Human wound healing related polypeptide SEQ ID NO 48.	953	99
1785	gi619730	Homo sapiens	nuclear factor I	953	99
1785	gi9653290	Mus sp.	NFI-X3	953	99
1786	gi13810568	Homo sapiens	Toll-like receptor 5	4482	100
1786	ABB11795	Homo sapiens	Human Toll/IL-1R-like protein homologue, SEQ ID NO:2165.	4478	99
1786	gi3132526	Homo sapiens	Toll/interleukin-1 receptor-like protein 3	4464	99

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SEQ ID	Hit ID	Species	Description	S score	% Identity
1787	AAB88597	Homo sapiens	Human hydrophobic domain containing protein clone HP03670 #121.	887	82
1787	AAB56473	Homo sapiens	Human prostate cancer antigen protein sequence SEQ ID NO:1051.	887	82
1787	AAB60119	Homo sapiens	Human transport protein TPPT-39.	564	75
1788	AAB80300	Homo sapiens	Human prostate cancer antigen #28.	741	89
1788	AAB80276	Homo sapiens	Human prostate cancer antigen #4.	741	89
1788	gi4929765	Homo sapiens	CGI-148 protein	741	89
1789	gi22038189	Escherichia coli	multidrug transporter	2265	100
1789	gi1736785	Escherichia coli	Acriflavin resistance protein F (EnvD protein).	2265	100
1789	gi15980819	Yersinia pestis	AcrB/AcrD/AcrF family membrane protein	1854	79
1790	gi17741602	ribose [Agrobacterium tumefaciens str. C58 (U. Washington)]	ABC transporter, membrane spanning protein	549	59
1790	gi15160166	Agrobacterium tumefaciens str. C58 (Cereon)	AGR_L_3181p	549	59
1790	gi20515187	Thermoanaerobacter tengcongensis	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	340	38
1791	gi1788573	Escherichia coli K12	sn-glycerol-3-phosphate permease	1073	100
1791	gi1799587	Escherichia coli	glycerol-3-phosphate transport protein	1073	100
1791	gi41587	Escherichia coli	glycerol-3-phosphatase transporter (AA 1 - 452, glpT)	1073	100
1792	gi1790233	Escherichia coli K12	arylsulfatase	679	98
1792	gi12518665	Escherichia coli O157:H7 EDL933	arylsulfatase	679	98
1792	gi13364207	Escherichia coli O157:H7	arylsulfatase	679	98
1793	gi21959134	Yersinia pestis KIM	sulfate transporter	378	80
1793	gi9657461	Vibrio cholerae	sulfate permease family protein	267	51
1793	gi18145142	Clostridium perfringens str. 13	probable sulfate permease	264	53
1794	gi1799719	PIR Accession Number S08346 [Escherichia coli]	similar to	922	100
1794	gi15156677	Agrobacterium tumefaciens str. C58 (Cereon)	AGR_C_2926p	452	50
1795	gi11177166	Mus musculus	adhesion molecule ninjurin	228	81
1795	gi3077901	Mus musculus	ninjurin	228	81
1795	gi1644366	Rattus norvegicus	ninjurin1	228	81

Table 2B

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SEQ ID	Hit ID	Species	Description	S score	% Identity
1796	AAU74824	Homo sapiens	Human REPTR 7 protein.	6196	92
1796	ABB90740	Homo sapiens	Human Tumour Endothelial Marker polypeptide SEQ ID NO 212.	6196	92
1796	ABB90725	Homo sapiens	Human Tumour Endothelial Marker polypeptide SEQ ID NO 188.	6196	92
1797	ABP61451	Homo sapiens	Human NF-kB activating protein SEQ ID NO 55.	1331	100
1797	AAV94343	Homo sapiens	Human cell surface receptor protein #10.	1331	100
1797	gi13938575	Homo sapiens	Similar to RIKEN cDNA 2610511E22 gene	1331	100
1798	gi606234	Escherichia coli	secY	953	100
1798	gi42989	Escherichia coli	SecY (PrIA) polypeptide (aa 1-443)	953	100
1798	gi16421976	Salmonella typhimurium LT2	preprotein translocase of IISF family	950	99
1799	gi18255305	Mus musculus	p53 apoptosis effector related to Pmp22	440	53
1799	gi7582391	Mus musculus	p53 apoptosis-associated target	440	53
1799	AAM50572	Homo sapiens	Human tumour suppressor protein THW.	391	100
1800	AAU11433	Homo sapiens	Human short-chain dehydrogenase, SCDR.	531	58
1800	AAU18368	Homo sapiens	Human endocrine polypeptide SEQ ID No 323.	531	58
1800	AAU18369	Homo sapiens	Human endocrine polypeptide SEQ ID No 324.	530	59
1801	ABB12425	Homo sapiens	Human bone marrow expressed protein SEQ ID NO: 264.	1781	90
1801	AAM50318	Homo sapiens	Human membrane transporter (MTP) 33556.	1499	90
1801	AAM83805	Homo sapiens	Human immune/haematopoietic antigen SEQ ID NO:11398.	1499	90
1802	gi20810074	Homo sapiens	Similar to pepsinogen 5, group I (pepsinogen A)	670	86
1802	AAB61351	Homo sapiens	Pepsin protein.	661	85
1802	AAB66589	Homo sapiens	Human pepsin.	661	85
1803	ABB04707	Homo sapiens	Human SP82 protein SEQ ID NO:2.	1113	99
1803	ABB84912	Homo sapiens	Human PRO1356 protein sequence SEQ ID NO:192.	1113	99
1803	AAU76534	Homo sapiens	Tumour-associated antigenic target protein, TAT134.	1113	99
1804	gi2641217	Oryctolagus cuniculus	anion exchanger 3 brain isoform	645	66
1804	gi476222	Homo sapiens	anion exchanger 3 brain isoform	645	66
1804	gi886256	Homo sapiens	anion exchange protein	642	66
1805	AAM25789	Homo sapiens	Human protein sequence SEQ ID NO:1304.	2659	56
1805	AAB29632	Homo sapiens	Human pollinosis-associated gene 581-encoded protein, SEQ ID NO:12.	2659	56
1805	gi18698435	Homo sapiens	pVHL-interacting deubiquitinating enzyme 1 type II	2659	56
1806	AAU29153	Homo sapiens	Human PRO polypeptide sequence #130.	1771	98

Table 2B

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SEQ ID	Hit ID	Species	Description	S score	% Identity
1806	AAV99363	Homo sapiens	Human PRO1380 (UNQ717) amino acid sequence SEQ ID NO:79.	1771	98
1806	AAG67487	Homo sapiens	Amino acid sequence of a human transporter protein.	1765	98
1807	ABB76315	Homo sapiens	Human protein phosphatase PP-8 Incyte ID No. 4022502CD1.	667	73
1807	gi15778670	Mus musculus	sphingosine-1-phosphate phosphatase	151	30
1807	gi9623190	Mus musculus	sphingosine-1-phosphate phosphohydrolase	151	30
1808	AAM93947	Homo sapiens	Human polypeptide, SEQ ID NO: 4138.	231	93
1808	AAM93886	Homo sapiens	Human polypeptide, SEQ ID NO: 4013.	231	93
1808	AAM93857	Homo sapiens	Human polypeptide, SEQ ID NO: 3949.	231	93
1809	gi14575679	Homo sapiens	hemicentin	597	95
1809	gi3328186	Caenorhabditis elegans	hemicentin precursor	354	57
1809	AAU75886	Homo sapiens	Human adhesion molecule protein AD4/AAD21820.1.	185	33
1810	gi3581982	Homo sapiens	extraneuronal monoamine transporter	775	99
1810	gi14270513	Homo sapiens	organic cation transporter 3	775	99
1810	gi13699874	Mus musculus	organic cation transporter 3	720	89
1811	AAB74762	Homo sapiens	Human secreted protein sequence encoded by gene 18 SEQ ID NO:71.	266	88
1811	AAB74760	Homo sapiens	Human secreted protein sequence encoded by gene 18 SEQ ID NO:69.	266	91
1811	AAB74759	Homo sapiens	Human secreted protein sequence encoded by gene 18 SEQ ID NO:68.	266	91
1812	gi15082375	Homo sapiens	Similar to transmembrane 7 superfamily member 1 (upregulated in kidney)	912	82
1812	gi13096836	Mus musculus	Similar to transmembrane 7 superfamily member 1 (upregulated in kidney)	885	80
1812	ABB97817	Homo sapiens	Human secretory polypeptide (SPTM) 69.	432	68
1813	gi1504024	Homo sapiens	similar to Mouse finger protein(clone mkr3)(S03677):	901	37
1813	gi14549186	Mus musculus	zinc finger protein 219	636	31
1813	AAM39029	Homo sapiens	Human polypeptide SEQ ID NO 2174.	619	32
1814	AAV53644	Homo sapiens	Protein encoded by the human longevity assurance gene 1 (LAG1).	1382	93
1814	AAR20230	Homo sapiens	hUOG-1.	1382	93
1814	gi4324468	Homo sapiens	LAG1 protein	1382	93
1815	AAU75907	Homo sapiens	Human epidermis-specific serine protease #2.	329	41
1815	gi6009515	Xenopus laevis	epidermis specific serine protease	329	41
1815	gi19353198	Mus musculus	RIKEN cDNA 2010001P08 gene	323	41
1816	AAM42401	Homo sapiens	Human polypeptide SEQ ID NO 134.	706	100
1816	gi1786232	Escherichia coli K12	K ⁺ efflux antiporter, glutathione-regulated	706	100
1816	gi21321928	Escherichia coli	Glutathione-regulated potassium-	706	100

Table 2B
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SEQ ID	Hit ID	Species	Description	S score	% Identity
			efflux system protein KefC (K(+)/H(+)) antiporter).		
1817	gi1657563	Escherichia coli	dioxygenase	1510	100
1817	gi1786565	Escherichia coli K12	taurine dioxygenase, 2-oxoglutarate-dependent	1510	100
1817	gi1054578	Escherichia coli	dioxygenase	1510	100
1818	gi1787550	Escherichia coli K12	homolog of Salmonella peptide transport permease protein	928	98
1818	gi12515484	Escherichia coli O157:H7 EDL933	homolog of Salmonella peptide transport permease protein	928	98
1818	gi13361335	Escherichia coli O157:H7	homolog of Salmonella peptide transport permease protein	928	98
1819	gi9652147	Homo sapiens	transmembrane-type protein tyrosine phosphatase H	5771	98
1819	gi475004	Homo sapiens	protein tyrosine phosphatase precursor	5235	93
1819	gi1321659	Rattus norvegicus	brain-enriched membrane-associated protein tyrosine phosphatase (BEM)-2	1487	71
1820	gi7141127	Homo sapiens	Ellis-van Creveld syndrome protein	1277	100
1820	gi7271903	Homo sapiens	DWF-1	1271	99
1820	gi13506715	Bos taurus	Ellis-van Creveld syndrome protein	1034	81
1821	AAG72370	Homo sapiens	Human OR-like polypeptide query sequence, SEQ ID NO: 2051.	568	98
1821	AAG71453	Homo sapiens	Human olfactory receptor polypeptide, SEQ ID NO: 1134.	568	98
1821	AAE04556	Homo sapiens	Human G-protein coupled receptor-12 (GCREC-12) protein.	558	100
1822	ABB89189	Homo sapiens	Human polypeptide SEQ ID NO 1565.	388	63
1822	AAM90349	Homo sapiens	Human immune/haematopoietic antigen SEQ ID NO:17942.	126	50
1822	AAB95094	Homo sapiens	Human protein sequence SEQ ID NO:17042.	94	41

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SEQ ID	Database entry ID	Description	Results*
912	BL01158	Macrophage migration inhibitory factor family proteins.	BL01158A 21.81 4.971e-37 124-169 BL01158B 17.07 4.343e-23 169-196
912	PF00043	Glutathione S-transferases.	PF00043 21.83 5.333e-14 377-407
913	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 8.200e-17 180-208 PD01719A 12.89 2.364e-13 123-151
913	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 2.091e-10 817-828
913	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 6.538e-16 812-828 BL01187B 12.04 5.696e-13 569-585 BL01187B 12.04 7.261e-13 696-712 BL01187A 9.98 1.429e-10 508-520 BL01187B 12.04 2.286e-10 484-500 BL01187A 9.98 1.750e-09 796-808
913	BL00022	EGF-like domain proteins.	BL00022B 7.54 1.900e-09 821-828
913	BL01177	Anaphylatoxin domain proteins.	BL01177D 17.50 5.167e-09 503-521
913	BL00281	Bowman-Birk serine protease inhibitors family proteins.	BL00281A 14.18 6.754e-09 479-496
913	BL00799	Granulins proteins.	BL00799B 11.02 7.429e-09 475-511
913	PR00907	THROMBOMODULIN SIGNATURE	PR00907B 11.29 2.479e-11 808-825 PR00907G 11.63 9.660e-10 812-839 PR00907G 11.63 9.745e-10 696-723 PR00907G 11.63 9.027e-09 569-596
914	BL01158	Macrophage migration inhibitory factor family proteins.	BL01158A 21.81 4.073e-33 2-47 BL01158B 17.07 2.884e-20 47-74
915	BL01158	Macrophage migration inhibitory factor family proteins.	BL01158B 17.07 4.343e-23 60-87 BL01158A 21.81 3.656e-22 2-47
916	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 5.091e-27 101-138
916	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134B 15.99 8.560e-17 626-650 BL00134A 11.96 1.321e-16 469-486 BL00134C 13.45 4.462e-16 662-676
916	BL01253	Type I fibronectin domain proteins.	BL01253C 15.89 9.027e-40 327-366 BL01253B 15.21 5.071e-38 272-316 BL01253H 13.15 7.070e-36 644-679 BL01253E 16.01 1.000e-34 543-580 BL01253F 14.35 2.846e-34 581-620 BL01253A 20.33 7.097e-25 201-230 BL01253G 11.34 8.085e-18 625-639 BL01253D 4.84 7.070e-16 469-483
916	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722A 12.27 3.793e-14 470-486 PR00722C 10.87 2.059e-13 625-638
916	BL00021	Kringle domain proteins.	BL00021D 24.56 3.000e-32 634-676 BL00021B 13.33 9.217e-17 469-487 BL00021C 22.21 4.293e-12 554-576
916	PR00013	FIBRONECTIN TYPE II REPEAT	PR00013C 12.29 4.273e-19 132-

Table 3A
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SEQ ID	Database entry ID	Description	Results*
		SIGNATURE	148 PR00013A 12.26 6.595e-11 105-115 PR00013B 14.75 1.409e-10 116-129
916	BL00495	Apple domain proteins.	BL00495N 11.04 7.987e-21 618-653 BL00495O 13.75 3.311e-17 653-682 BL00495M 8.50 6.243e-10 545-580
916	BL00022	EGF-like domain proteins.	BL00022B 7.54 1.900e-09 267-274
916	PR00018	KRINGLE DOMAIN SIGNATURE	PR00018C 14.30 7.750e-22 331-352 PR00018A 14.52 2.286e-12 286-302 PR00018B 17.75 7.818e-10 302-315 PR00018D 13.51 3.531e-09 356-368
916	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010A 11.79 4.000e-09 160-172 PR00010C 11.16 8.071e-09 182-193
916	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 8.826e-09 179-198
916	PD00919	CALCIUM-BINDING PRECURSOR SIGNAL R.	PD00919A 11.53 1.000e-08 164-176
917	BL01248	Laminin-type EGF-like (LE) domain proteins.	BL01248 11.02 4.429e-15 314-327 BL01248 11.02 1.375e-14 379-392 BL01248 11.02 7.975e-11 1011-1024 BL01248 11.02 5.245e-09 1069-1082 BL01248 11.02 5.585e-09 899-912
917	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011A 14.06 8.579e-19 1060-1079 PR00011D 14.03 9.250e-17 1107-1126 PR00011B 13.08 7.938e-16 846-865 PR00011A 14.06 1.340e-15 535-554 PR00011D 14.03 3.800e-15 846-865 PR00011A 14.06 5.755e-15 846-865 PR00011B 13.08 5.846e-15 1107-1126 PR00011D 14.03 2.286e-14 1060-1079 PR00011B 13.08 2.333e-14 485-504 PR00011B 13.08 6.333e-14 1060-1079 PR00011D 14.03 7.429e-14 485-504 PR00011B 13.08 1.458e-13 535-554 PR00011D 14.03 1.849e-13 535-554 PR00011A 14.06 3.593e-13 1107-1126 PR00011A 14.06 7.254e-13 485-504 PR00011B 13.08 9.847e-13 798-817 PR00011A 14.06 1.581e-12 798-817 PR00011C 24.25 7.623e-12 817-846 PR00011D 14.03 1.148e-11 798-817 PR00011A 14.06 3.492e-11 433-452 PR00011D 14.03 9.262e-11 433-452 PR00011C 24.25 8.800e-10 440-469 PR00011C 24.25 3.143e-09 455-484 PR00011B 13.08 6.548e-09 433-452
917	PD00320	LAMININ CHAIN EGF-LIKE	PD00320A 14.49 4.115e-10 813-

Table 3A
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SEQ ID	Database entry ID	Description	Results*
		DOMAIN P.	827 PD00320A 14.49 8.071e-09 1075-1089
918	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 2.636e-10 132-143
918	BL00790	Receptor tyrosine kinase class V proteins.	BL00790E 29.58 4.621e-10 666-714
918	BL01177	Anaphylatoxin domain proteins.	BL01177E 20.64 6.203e-12 377-404 BL01177D 17.50 3.000e-09 277-295 BL01177C 17.39 4.000e-09 121-140
918	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 8.412e-15 379-395 BL01187B 12.04 5.304e-13 299-315 BL01187B 12.04 7.652e-13 339-355 BL01187B 12.04 8.826e-13 127-143 BL01187B 12.04 6.000e-12 46-62 BL01187B 12.04 5.200e-11 258-274 BL01187B 12.04 6.400e-10 86-102 BL01187A 9.98 8.286e-10 110-122 BL01187A 9.98 5.125e-09 282-294 BL01187A 9.98 6.250e-09 68-80 BL01187A 9.98 8.125e-09 323-335
918	PR00907	THROMBOMODULIN SIGNATURE	PR00907G 11.63 6.774e-10 46-73 PR00907B 11.29 7.545e-10 215-232 PR00907G 11.63 9.321e-10 379-406 PR00907B 11.29 7.805e-09 82-99 PR00907B 11.29 9.232e-09 335-352 PR00907D 5.59 9.427e-09 344-370
919	BL00335	Parathyroid hormone family proteins.	BL00335B 24.23 1.000e-40 133-182 BL00335A 17.98 8.393e-39 80-115
920	BL01177	Anaphylatoxin domain proteins.	BL01177C 17.39 4.508e-10 92-111
920	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 8.043e-13 12-28 BL01187B 12.04 1.000e-11 139-155 BL01187A 9.98 1.474e-11 82-94 BL01187B 12.04 4.900e-11 98-114 BL01187A 9.98 7.429e-10 122-134
920	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011A 14.06 2.964e-14 288-307 PR00011B 13.08 4.356e-13 288-307 PR00011D 14.03 6.434e-13 376-395 PR00011B 13.08 2.887e-12 376-395 PR00011D 14.03 5.421e-12 288-307 PR00011D 14.03 5.721e-11 331-350 PR00011B 13.08 5.826e-10 331-350 PR00011A 14.06 8.957e-10 376-395
920	DM00864	EGF-LIKE DOMAIN.	DM00864A 15.21 3.314e-09 232-253
920	PR00764	COMPLEMENT C9 SIGNATURE	PR00764F 16.89 5.675e-09 236-257
920	BL00022	EGF-like domain proteins.	BL00022B 7.54 7.300e-09 67-74
920	BL00799	Granulins proteins.	BL00799H 14.15 9.083e-09 227-268

Table 3A
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SEQ ID	Database entry ID	Description	Results*
920	PR00907	THROMBOMODULIN SIGNATURE	PR00907B 11.29 8.714e-10 54-71 PR00907B 11.29 9.561e-09 135-152
920	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 1.000e-08 387-430
921	BL00472	Small cytokines (intercrine/chemokine) C-C subfamily signatur.	BL00472B 14.67 2.000e-16 35-53 BL00472A 7.45 4.724e-09 1-13
922	BL00132	Zinc carboxypeptidases, zinc-binding region 1 proteins.	BL00132C 21.35 1.837e-25 227-268 BL00132A 26.07 9.791e-24 149-190 BL00132E 17.72 2.350e-22 297-324 BL00132F 13.26 5.313e-18 325-347 BL00132B 15.93 5.065e-16 197-211 BL00132G 10.94 6.318e-14 382-400 BL00132D 12.70 5.313e-12 271-286
922	PR00765	CARBOXYPEPTIDASE A METALLOPROTEASE (M14) FAMILY SIGNATURE	PR00765B 15.57 2.875e-15 197-212 PR00765D 14.16 8.412e-15 330-344 PR00765C 12.55 2.432e-09 277-286
923	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 3.618e-25 93-130 BL00514E 14.28 8.286e-14 153-170 BL00514D 15.35 2.915e-12 134-147 BL00514G 15.98 4.444e-12 223-253
927	BL00453	FKBP-type peptidyl-prolyl cis-trans isomerase proteins.	BL00453B 23.86 8.500e-20 80-114 BL00453A 15.57 1.000e-15 55-70 BL00453C 9.72 8.650e-11 109-122
937	BL00796	14-3-3 proteins.	BL00796C 17.44 6.250e-38 143-193 BL00796B 10.67 1.514e-36 77-110 BL00796D 17.39 5.696e-34 194-240 BL00796E 14.15 7.353e-29 242-278
937	PR00305	14-3-3 PROTEIN ZETA SIGNATURE	PR00305F 15.95 3.250e-37 248-278 PR00305A 9.33 1.500e-33 77-107 PR00305D 16.34 6.400e-29 194-221 PR00305C 8.68 1.000e-28 159-182 PR00305B 9.99 4.375e-23 126-151 PR00305E 13.01 3.571e-10 221-248
938	BL00303	S-100/ICaBP type calcium binding protein.	BL00303A 21.77 9.526e-31 64-101 BL00303B 26.15 5.737e-30 111-148
938	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 9.471e-11 123-136
940	PD02365	CHAIN FACTOR INTERLEUKIN-12 BETA PRECURSOR IL-1.	PD02365C 7.89 6.680e-10 342-372
940	DM00202	w T-CELL IG HEAVY ALPHA.	DM00202A 9.44 9.813e-09 34-44
944	BL00284	Serpins proteins.	BL00284C 28.56 6.400e-25 319-361 BL00284E 19.15 1.000e-15 508-533 BL00284A 15.64 2.742e-15 200-224 BL00284B 17.99 6.182e-12 292-313 BL00284D 16.34 7.070e-12 430-457
944	PD02080	T-CELL GLYCOPROTEIN CD8 CHAIN SURFACE ALPHA PRE.	PD02080A 10.03 9.750e-10 35-51

Table 3A
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SEQ ID	Database entry ID	Description	Results*
944	PR00743	GLYCOSYL HYDROLASE FAMILY 36 SIGNATURE	PR00743B 14.95 8.831e-09 240-261
947	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 4.750e-17 552-565
947	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 2.373e-09 203-257
947	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.000e-09 559-568
947	BL00422	Granins proteins.	BL00422E 26.86 8.615e-09 462-498
950	PR00356	TYPE II ANTIFREEZE PROTEIN SIGNATURE	PR00356D 13.09 8.038e-09 174-191
951	BL00615	C-type lectin domain proteins.	BL00615A 16.68 4.316e-13 209-227
951	PR00356	TYPE II ANTIFREEZE PROTEIN SIGNATURE	PR00356B 14.85 6.294e-10 209-227 PR00356A 12.90 7.188e-10 197-210
952	BL00570	Bacterial ring hydroxylating dioxygenases alpha-subunit signa.	BL00570B 19.03 9.357e-09 271-303
953	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 1.931e-09 72-93
953	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 3.571e-09 107-120
953	BL00415	Synapsins proteins.	BL00415N 4.29 5.730e-09 13-57
954	PR00901	PHEROMONE B ALPHA-1 RECEPTOR SIGNATURE	PR00901H 14.99 4.706e-09 56-67
958	PR00138	MATRIXIN SIGNATURE	PR00138C 16.41 6.478e-32 178-207 PR00138D 16.56 1.360e-28 236-262 PR00138B 15.82 8.071e-18 155-171 PR00138A 15.14 5.091e-16 108-122 PR00138E 6.01 9.250e-15 269-283
958	BL00024	Hemopexin domain proteins.	BL00024C 22.98 1.000e-40 177-226 BL00024B 21.53 2.636e-33 129-163 BL00024D 17.28 4.086e-31 230-262 BL00024F 11.30 2.731e-22 305-326 BL00024H 11.35 1.947e-14 411-423 BL00024E 7.58 5.500e-14 269-283 BL00024G 13.31 4.115e-13 342-355 BL00024A 11.49 5.050e-13 108-119
958	BL00142	Neutral zinc metalloproteinases, zinc-binding region proteins.	BL00142 8.38 3.455e-11 236-247
958	PR00480	ASTACIN FAMILY SIGNATURE	PR00480B 15.41 1.643e-09 231-250
958	BL00546	Matrixins cysteine switch.	BL00546B 20.11 1.000e-40 178-222 BL00546C 16.41 1.771e-31 230-262 BL00546A 19.62 5.304e-28 88-118 BL00546E 10.23 3.323e-22 305-326 BL00546G 16.84 7.300e-19 363-383 BL00546D 10.34 1.486e-14 269-283 BL00546F 12.40 2.800e-13 342-355 BL00546H 10.76 6.625e-12 458-469 BL00546H 10.76

Table 3A

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SEQ ID	Database entry ID	Description	Results*
			4.512e-09 411-422
959	PD02043	RIBULOSE BISPHOSPHATE CARBOXYLAS.	PD02043A 12.92 5.800e-09 137-171
962	BL00598	Chromo domain proteins.	BL00598 14.45 5.781e-16 63-85
962	PR00504	CHROMODOMAIN SIGNATURE	PR00504C 11.19 5.186e-10 72-85 PR00504B 9.12 3.250e-09 57-72
967	PF00420	NADH-ubiquinone/plastoquinone oxidoreductase chain 4L.	PF00420A 16.63 9.526e-10 89-120
967	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245C 7.84 5.000e-16 185-201 PR00245A 18.03 6.878e-16 59-81 PR00245D 10.47 8.500e-15 221-233 PR00245E 12.40 1.000e-09 238-253
967	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237A 11.48 5.065e-09 26-51
967	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 2.184e-12 90-130 BL00237D 11.23 5.909e-09 229-246
968	BL00059	Zinc-containing alcohol dehydrogenases proteins.	BL00059B 16.08 5.705e-14 223-251
968	BL01162	Quinone oxidoreductase / zeta-crystallin proteins.	BL01162C 22.80 5.846e-14 284-328 BL01162B 18.11 4.205e-11 223-251 BL01162A 15.38 3.805e-09 194-217
970	PF00676	Dehydrogenase E1 component.	PF00676B 24.71 2.800e-39 257-295 PF00676D 14.40 7.545e-24 341-361 PF00676C 16.88 5.737e-23 309-333 PF00676A 12.85 5.050e-12 131-144
970	BL00801	Transketolase proteins.	BL00801D 22.48 7.750e-11 250-290
977	PR00457	ANIMAL HAEM PEROXIDASE SIGNATURE	PR00457E 20.67 9.591e-26 409-436 PR00457D 16.81 5.667e-22 384-405 PR00457G 17.45 1.000e-15 590-611 PR00457B 13.29 4.343e-15 216-232 PR00457C 19.25 3.250e-12 366-385 PR00457A 15.80 5.645e-12 162-174 PR00457H 15.90 1.900e-10 684-699 PR00457F 13.69 6.800e-09 461-472
978	BL00269	Mammalian defensins proteins.	BL00269C 16.52 3.942e-17 95-124 BL00269B 19.17 4.122e-15 57-86 BL00269A 8.53 3.250e-13 31-51
982	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 8.297e-10 79-113
985	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 9.663e-09 78-106
987	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 1.000e-09 247-261 PR00019B 11.36 2.080e-09 316-330 PR00019B 11.36 3.160e-09 244-258 PR00019B 11.36 4.240e-09 100-114 PR00019B 11.36 5.680e-09 148-162
988	BL01215	Mrp family proteins.	BL01215C 18.97 6.447e-36 191-233 BL01215D 30.07 1.000e-33

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SEQ ID	Database entry ID	Description	Results*
			250-300 BL01215A 9.75 4.400e-22 101-128 BL01215B 9.34 2.658e-13 134-147
988	PR00364	DISEASE RESISTANCE PROTEIN SIGNATURE	PR00364A 8.19 2.023e-09 105-121
988	BL00746	NifH/frxC family proteins.	BL00746A 24.43 2.819e-09 107-152
988	PR00091	NITROGENASE COMPONENT II SIGNATURE	PR00091A 8.10 4.329e-09 109-123
988	BL01128	Shikimate kinase proteins.	BL01128A 18.84 8.221e-09 106-140
989	PF00094	von Willebrand factor type D domain proteins.	PF00094B 10.43 6.400e-17 491-509
989	PF00054	Laminin G domain proteins.	PF00054B 16.61 7.300e-09 658-670
989	BL00779	Glycoprotein hormones alpha chain proteins.	BL00779A 14.01 7.840e-09 329-356
989	BL01185	C-terminal cystine knot proteins.	BL01185B 21.14 9.153e-09 238-287
992	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 8.986e-11 78-112
992	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 2.000e-09 154-177
994	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 4.692e-11 148-172
994	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e-09 101-111
994	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870D 15.74 9.234e-09 274-309
995	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009D 14.19 4.300e-20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e-11 159-175
995	PR00837	ALLERGEN V5/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 6.143e-20 126-143 PR00837A 14.77 1.973e-13 57-76 PR00837D 11.12 3.700e-11 160-174
995	PR00838	VENOM ALLERGEN 5 SIGNATURE	PR00838G 16.07 2.033e-17 125-145 PR00838D 8.73 4.214e-09 57-76
996	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270B 22.18 5.567e-18 111-148 PD01270C 19.54 1.167e-17 154-183 PD01270A 17.22 4.960e-14 57-97 PD01270D 24.66 4.284e-09 188-224
999	BL01305	moaA / nifB / pqqE family proteins.	BL01305D 14.97 7.279e-09 7-22
1000	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.600e-12 42-65 BL00290B 13.17 1.474e-11 98-116
1002	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.846e-15 285-298 PD00066 13.92 1.600e-14 201-214 PD00066 13.92 2.800e-14 313-326 PD00066 13.92 2.000e-13 341-354 PD00066 13.92 5.500e-13 229-242 PD00066 13.92 8.435e-11 257-270
1002	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.471e-14 269-286 BL00028 16.07 3.769e-11 241-258

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SEQ ID	Database entry ID	Description	Results*
			BL00028 16.07 7.577e-11 325-342 BL00028 16.07 7.577e-11 353-370 BL00028 16.07 6.700e-10 185-202 BL00028 16.07 1.257e-09 297-314
1002	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-12 266-280 PR00048A 10.52 3.118e-12 238-252 PR00048A 10.52 8.941e-12 294-308 PR00048B 6.02 2.688e-10 310-320 PR00048B 6.02 3.250e-10 198-208 PR00048A 10.52 3.348e-10 322-336 PR00048A 10.52 3.739e-10 210-224 PR00048A 10.52 5.696e-10 350-364 PR00048A 10.52 1.000e-09 182-196 PR00048B 6.02 1.947e-09 282-292 PR00048B 6.02 5.737e-09 338-348
1003	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.706e-14 607-624 BL00028 16.07 6.400e-13 411-428 BL00028 16.07 9.550e-13 579-596 BL00028 16.07 1.000e-12 439-456 BL00028 16.07 1.391e-12 495-512 BL00028 16.07 1.783e-12 523-540 BL00028 16.07 7.652e-12 383-400 BL00028 16.07 9.217e-12 355-372 BL00028 16.07 9.217e-12 663-680 BL00028 16.07 5.846e-11 467-484 BL00028 16.07 6.538e-11 635-652 BL00028 16.07 2.800e-10 327-344 BL00028 16.07 6.143e-09 262-279
1003	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e-15 399-412 PD00066 13.92 8.615e-15 343-356 PD00066 13.92 1.600e-14 427-440 PD00066 13.92 2.800e-14 511-524 PD00066 13.92 2.800e-14 623-636 PD00066 13.92 5.200e-14 595-608 PD00066 13.92 6.400e-14 567-580 PD00066 13.92 8.800e-14 371-384 PD00066 13.92 7.000e-13 315-328 PD00066 13.92 9.000e-13 483-496 PD00066 13.92 6.870e-11 455-468 PD00066 13.92 7.600e-09 539-552 PD00066 13.92 7.900e-09 651-664
1003	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 9.182e-15 492-506 PR00048A 10.52 1.750e-14 408-422 PR00048A 10.52 7.000e-14 576-590 PR00048A 10.52 1.000e-13 604-618 PR00048A 10.52 3.571e-13 380-394 PR00048A 10.52 4.214e-13 464-478 PR00048A 10.52 5.235e-12 352-366 PR00048B 6.02 1.000e-11 424-434 PR00048B 6.02 1.692e-11 340-350 PR00048B 6.02 7.231e-11 536-546 PR00048B 6.02 7.231e-11 620-630 PR00048A 10.52 8.579e-

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SEQ ID	Database entry ID	Description	Results*
			11 259-273 PR00048A 10.52 9.053e-11 436-450 PR00048B 6.02 9.308e-11 508-518 PR00048B 6.02 1.563e-10 592-602 PR00048B 6.02 2.125e-10 396-406 PR00048A 10.52 4.130e-10 660-674 PR00048A 10.52 4.522e-10 520- 534 PR00048A 10.52 6.478e-10 324-338 PR00048B 6.02 1.474e-09 564-574 PR00048B 6.02 2.421e-09 676-686 PR00048A 10.52 2.800e- 09 548-562 PR00048A 10.52 2.800e-09 632-646 PR00048B 6.02 2.895e-09 368-378 PR00048B 6.02 1.000e-08 648-658
1007	BL00478	LIM domain proteins.	BL00478B 14.79 3.739e-14 469- 484 BL00478B 14.79 3.500e-12 411-426 BL00478B 14.79 6.000e- 12 536-551
1007	DM00984	w MYOD MYOBLAST DETERMINATION SHORT.	DM00984B 15.18 4.822e-25 426- 481 DM00984C 7.66 8.036e-11 481-495
1007	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 7.022e-09 260-309
1008	DM00475	w LOW TRANSPOSASE SAPA 12K.	DM00475B 12.12 8.269e-09 115- 135
1011	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456F 5.86 6.400e-12 76-88
1012	PF00756	Putative esterase.	PF00756C 14.12 7.692e-10 103- 133
1016	PR00310	ANTI-PROLIFERATIVE PROTEIN BTG1 FAMILY SIGNATURE	PR00310D 9.10 1.540e-37 183-213 PR00310C 12.74 5.286e-35 153- 183 PR00310A 11.17 7.000e-27 16-41 PR00310E 13.58 6.914e-24 229-249 PR00310B 10.59 3.687e- 23 123-153
1016	BL00960	BTG1 family proteins.	BL00960B 24.47 3.288e-26 116- 161 BL00960C 12.68 3.647e-26 180-202 BL00960A 10.98 5.304e- 12 14-26
1017	PD01066	PROTEIN ZINC FINGER ZINC- FINGER METAL-BINDING NU.	PD01066 19.43 6.143e-32 44-83
1017	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.063e-15 523-540 BL00028 16.07 7.188e-15 383-400 BL00028 16.07 3.700e-13 467-484 BL00028 16.07 5.950e-13 439-456 BL00028 16.07 8.650e-13 271-288 BL00028 16.07 4.115e-11 355-372 BL00028 16.07 6.885e-11 327-344 BL00028 16.07 2.800e-10 411-428 BL00028 16.07 3.100e-10 495-512
1017	PD00066	PROTEIN ZINC-FINGER METAL- BINDI.	PD00066 13.92 6.625e-18 399-412 PD00066 13.92 2.385e-15 371-384 PD00066 13.92 8.615e-15 343-356 PD00066 13.92 3.500e-13 511-524 PD00066 13.92 1.000e-12 483-496

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SEQ ID	Database entry ID	Description	Results*
			PD00066 13.92 1.000e-11 427-440 PD00066 13.92 3.769e-10 455-468 PD00066 13.92 5.800e-09 539-552
1017	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.727e-15 520-534 PR00048A 10.52 1.750e-14 380-394 PR00048A 10.52 3.250e-14 408-422 PR00048A 10.52 4.857e-13 464-478 PR00048A 10.52 1.529e-12 436-450 PR00048A 10.52 2.059e-12 352-366 PR00048B 6.02 3.769e-11 368-378 PR00048B 6.02 5.846e-11 396-406 PR00048B 6.02 5.846e-11 508-518 PR00048A 10.52 1.783e-10 492-506 PR00048B 6.02 8.313e-10 480-490 PR00048A 10.52 4.240e-09 324-338 PR00048B 6.02 5.737e-09 340-350 PR00048A 10.52 8.200e-09 146-160
1020	BL00478	LIM domain proteins.	BL00478B 14.79 6.000e-15 219-234 BL00478B 14.79 8.250e-12 99-114 BL00478B 14.79 8.250e-12 160-175 BL00478B 14.79 2.800e-11 282-297
1024	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.400e-38 17-56
1024	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.600e-14 230-243 PD00066 13.92 8.200e-14 286-299 PD00066 13.92 8.200e-14 398-411 PD00066 13.92 1.000e-13 342-355 PD00066 13.92 6.478e-11 314-327 PD00066 13.92 6.478e-11 370-383 PD00066 13.92 6.870e-11 258-271
1024	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.850e-13 354-371 BL00028 16.07 4.522e-12 242-259 BL00028 16.07 8.826e-12 214-231 BL00028 16.07 9.609e-12 270-287 BL00028 16.07 2.731e-11 326-343 BL00028 16.07 1.900e-10 382-399 BL00028 16.07 8.500e-10 298-315 BL00028 16.07 5.629e-09 410-427
1024	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479A 19.86 7.319e-09 201-224
1024	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.273e-15 351-365 PR00048A 10.52 5.500e-13 239-253 PR00048A 10.52 5.500e-13 267-281 PR00048A 10.52 8.941e-12 323-337 PR00048A 10.52 5.263e-11 379-393 PR00048A 10.52 1.783e-10 407-421 PR00048B 6.02 3.250e-10 339-349 PR00048B 6.02 8.875e-10 227-237 PR00048B 6.02 1.000e-09 283-293 PR00048B 6.02 1.000e-09 395-405 PR00048A 10.52 1.360e-

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SEQ ID	Database entry ID	Description	Results*
			09 295-309 PR00048B 6.02 2.895e-09 423-433 PR00048A 10.52 7.480e-09 211-225
1025	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.	BL00824B 9.21 4.892e-09 394-414
1025	PR00966	POTYVIRUS NUCLEAR INCLUSION A CYSTEINE PROTEASE (C4) SIGNATURE	PR00966H 13.17 9.727e-09 215-235
1026	BL01282	BIR repeat proteins.	BL01282B 30.49 3.829e-09 12-51
1026	PF00992	Troponin.	PF00992A 16.67 5.263e-09 136-171
1026	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 8.333e-09 31-40
1029	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 5.613e-09 171-199
1029	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 5.213e-10 91-137 BL00203 13.94 5.041e-09 71-117 BL00203 13.94 8.898e-09 53-99
1031	BL00170	Cyclophilin-type peptidyl-prolyl cis-trans isomerase signatur.	BL00170B 20.97 1.000e-40 48-88 BL00170C 18.49 1.000e-40 95-140 BL00170A 17.08 2.452e-16 18-45
1031	PR00153	CYCLOPHILIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SIGNATURE	PR00153C 11.01 4.375e-20 96-112 PR00153B 11.57 1.500e-17 53-66 PR00153E 9.10 7.632e-17 124-140 PR00153D 11.99 6.400e-16 111-124 PR00153A 12.98 3.093e-11 24-40
1031	PF00638	RanBP1 domain proteins.	PF00638 11.91 5.569e-09 68-83
1035	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.149e-29 6-45
1035	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.692e-15 234-247 PD00066 13.92 3.077e-15 374-387 PD00066 13.92 3.077e-15 458-471 PD00066 13.92 5.846e-15 486-499 PD00066 13.92 3.400e-14 150-163 PD00066 13.92 5.800e-14 206-219 PD00066 13.92 5.800e-14 290-303 PD00066 13.92 5.800e-14 318-331 PD00066 13.92 8.800e-14 514-527 PD00066 13.92 3.500e-13 346-359 PD00066 13.92 7.500e-13 402-415 PD00066 13.92 8.714e-12 178-191 PD00066 13.92 3.700e-09 430-443 PD00066 13.92 5.500e-09 262-275
1035	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.750e-14 215-229 PR00048A 10.52 4.750e-14 467-481 PR00048A 10.52 7.000e-14 355-369 PR00048A 10.52 4.857e-13 299-313 PR00048A 10.52 5.500e-13 99-113 PR00048A 10.52 5.500e-13 327-341 PR00048A 10.52 1.000e-12 495-509 PR00048A 10.52 2.059e-12 271-285 PR00048A 10.52 2.588e-12 523-537 PR00048A 10.52 8.412e-12 243-257 PR00048A

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SEQ ID	Database entry ID	Description	Results*
			10.52 4.316e-11 131-145 PR00048B 6.02 4.462e-11 115-125 PR00048A 10.52 8.579e-11 439-453 PR00048A 10.52 9.053e-11 383-397 PR00048A 10.52 1.391e-10 159-173 PR00048B 6.02 1.563e-10 455-465 PR00048A 10.52 3.739e-10 411-425 PR00048B 6.02 6.625e-10 203-213 PR00048B 6.02 6.625e-10 287-297 PR00048A 10.52 3.160e-09 551-565 PR00048A 10.52 4.600e-09 187-201 PR00048B 6.02 8.579e-09 147-157
1035	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.900e-13 358-375 BL00028 16.07 2.350e-13 102-119 BL00028 16.07 8.826e-12 470-487 BL00028 16.07 2.038e-11 554-571 BL00028 16.07 5.500e-11 190-207 BL00028 16.07 5.846e-11 274-291 BL00028 16.07 6.192e-11 218-235 BL00028 16.07 8.269e-11 330-347 BL00028 16.07 1.300e-10 526-543 BL00028 16.07 1.600e-10 414-431 BL00028 16.07 3.700e-10 386-403 BL00028 16.07 6.700e-10 442-459 BL00028 16.07 7.000e-10 302-319 BL00028 16.07 1.000e-09 134-151 BL00028 16.07 3.314e-09 246-263 BL00028 16.07 1.000e-08 498-515
1038	BL01130	Sulfate transporters proteins.	BL01130A 21.63 7.407e-25 331-385 BL01130B 23.34 2.286e-23 429-481
1038	DM01292	ESICULAR LUMEN DOMAIN.	DM01292I 12.82 9.400e-10 148-190 DM01292I 12.82 9.400e-10 591-633
1042	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327B 19.84 5.574e-10 169-191
1042	PD02365	CHAIN FACTOR INTERLEUKIN-12 BETA PRECURSOR IL-1.	PD02365C 7.89 4.196e-09 365-395
1043	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 3.500e-15 142-158 BL00983B 8.19 1.643e-12 84-94 BL00983A 5.84 7.261e-10 74-83
1047	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 6.400e-22 281-299 BL00290A 20.89 4.600e-16 34-57 BL00290A 20.89 2.080e-10 224-247
1051	BL01221	PMP-22 / EMP / MP20 family proteins.	BL01221B 13.29 6.745e-09 54-68
1052	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 4.981e-09 46-62
1052	BL00272	Snake toxins proteins.	BL00272C 8.27 8.326e-09 50-62
1054	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 4.627e-30 723-778 BL00420C 11.90 9.100e-13 809-820
1054	PR00258	SPERACT RECEPTOR SIGNATURE	PR00258B 9.63 3.813e-15 738-750 PR00258E 13.33 2.047e-12 808-

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SEQ ID	Database entry ID	Description	Results*
			821 PR00258C 9.05 2.837e-10 753-764
1054	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514G 15.98 4.326e-09 542-572
1055	BL01212	ATP P2X receptors proteins.	BL01212A 34.89 1.000e-40 41-94 BL01212E 24.87 1.000e-40 225-280 BL01212G 11.86 3.700e-34 309-337 BL01212D 11.42 9.609e-27 182-206 BL01212B 19.25 8.393e-21 126-151 BL01212F 10.12 2.421e-15 290-301 BL01212C 8.40 2.500e-14 158-169
1056	PR00920	SPUMAVIRUS ASPARTIC PROTEASE (A9) SIGNATURE	PR00920C 13.24 7.310e-09 149-171
1057	BL00682	ZP domain proteins.	BL00682C 20.71 1.706e-12 439-464
1057	BL00025	P-type 'Trefoil' domain proteins.	BL00025 17.17 5.645e-09 231-252
1059	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 4.273e-14 98-138
1059	PR00854	PROSTAGLANDIN D RECEPTOR SIGNATURE	PR00854E 10.50 4.649e-26 236-260 PR00854B 7.30 8.154e-21 41-59 PR00854G 10.66 1.783e-18 341-358 PR00854D 9.41 2.500e-18 185-201 PR00854A 15.24 9.077e-18 6-21 PR00854H 14.71 6.203e-17 369-390 PR00854C 12.92 1.643e-12 93-105 PR00854F 12.83 9.682e-11 321-333
1059	PR00856	PROSTACYCLIN (PROSTANOID IP) RECEPTOR SIGNATURE	PR00856E 9.82 1.724e-09 178-195
1060	BL01271	Sodium:sulfate symporter family proteins.	BL01271D 25.26 1.000e-40 480-535 BL01271B 12.02 6.400e-24 208-233 BL01271A 8.06 7.955e-23 132-152 BL01271C 13.62 7.429e-20 407-429
1062	PF00798	Arenavirus glycoprotein.	PF00798I 18.55 8.811e-09 53-90
1064	BL01017	Ergosterol biosynthesis ERG4/ERG24 family proteins.	BL01017D 20.82 1.000e-40 232-278 BL01017F 23.34 9.196e-35 291-344 BL01017C 15.91 7.324e-23 181-207 BL01017B 12.69 9.419e-17 166-181
1065	BL00874	Bacterial type II secretion system protein F proteins.	BL00874B 29.89 9.724e-09 414-469
1066	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270C 19.54 2.895e-16 43-72
1066	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 8.435e-09 183-193
1067	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 3.455e-14 77-117
1067	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237C 15.69 1.257e-10 91-114 PR00237E 13.03 9.100e-10 175-199
1067	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245A 18.03 9.581e-18 46-68 PR00245C 7.84 4.780e-13 214-230 PR00245E 12.40 6.741e-09 267-282
1067	PR00534	MELANOCORTIN RECEPTOR FAMILY SIGNATURE	PR00534A 11.49 9.229e-09 38-51

Table 3A
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SEQ ID	Database entry ID	Description	Results*
1069	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 5.909e-15 409-440 BL00107B 13.31 4.214e-11 484-500
1069	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109E 14.41 4.353e-09 549-572
1071	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.789e-13 222-245
1072	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.892e-10 4-14 PR00308C 3.83 8.892e-10 5-15 PR00308C 3.83 8.013e-09 3-13
1072	PR00698	C.ELEGANS SRG FAMILY INTEGRAL MEMBRANE PROTEIN SIGNATURE	PR00698E 14.43 8.714e-09 111-137
1075	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e-11 69-85 PF00023B 14.20 2.636e-09 131-141
1075	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 6.087e-09 128-141
1075	PR00806	VINCULIN SIGNATURE	PR00806C 11.07 8.839e-09 350-368
1075	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.505e-09 135-190 PF00791B 28.49 9.835e-09 69-124
1076	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 5.610e-11 174-214 BL00237C 13.19 4.176e-10 317-344
1076	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237F 13.57 7.677e-11 322-347 PR00237E 13.03 6.100e-10 276-300 PR00237A 11.48 8.839e-09 103-128
1077	BL00216	Sugar transport proteins.	BL00216B 27.64 1.831e-09 139-189
1079	BL00462	Gamma-glutamyltranspeptidase proteins.	BL00462A 20.89 4.000e-20 108-151 BL00462D 23.07 7.256e-12 356-396 BL00462B 17.88 9.153e-12 183-220
1080	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 2.125e-09 1363-1412 BL00115Z 3.12 6.096e-09 1349-1398
1083	BL00272	Snake toxins proteins.	BL00272C 8.27 9.182e-10 109-121
1083	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.348e-14 366-397 BL00107B 13.31 4.176e-09 441-457
1083	PR00653	ACTIVIN TYPE II RECEPTOR SIGNATURE	PR00653D 13.25 7.200e-09 385-407
1083	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109E 14.41 6.727e-11 535-558 PR00109D 17.04 7.609e-09 442-465
1083	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 9.135e-09 105-121
1084	BL00272	Snake toxins proteins.	BL00272C 8.27 9.182e-10 109-121
1084	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.348e-14 428-459 BL00107B 13.31 4.176e-09 503-519
1084	PR00653	ACTIVIN TYPE II RECEPTOR SIGNATURE	PR00653D 13.25 7.200e-09 447-469

Table 3A
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SEQ ID	Database entry ID	Description	Results*
1084	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109E 14.41 6.727e-11 597-620 PR00109D 17.04 7.609e-09 504-527
1084	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 9.135e-09 105-121
1085	PR00541	MUSCARINIC M4 RECEPTOR SIGNATURE	PR00541C 8.06 7.726e-09 486-507
1086	PR00541	MUSCARINIC M4 RECEPTOR SIGNATURE	PR00541C 8.06 7.726e-09 755-776
1087	PD01101	INHIBITOR HEAVY CHAIN CHANNEL IN.	PD01101B 21.53 3.318e-22 343-396
1088	BL00129	Glycosyl hydrolases family 31 proteins.	BL00129A 26.21 2.400e-28 114-160 BL00129D 16.76 6.806e-26 364-408 BL00129C 15.12 5.295e-24 326-354 BL00129E 22.60 4.857e-23 428-464 BL00129B 19.19 4.436e-15 225-252 BL00129F 26.19 2.500e-13 544-582
1090	PR00887	STRUCTURE-SPECIFIC RECOGNITION PROTEIN SIGNATURE	PR00887A 11.39 1.643e-22 343-360 PR00887F 12.74 2.000e-22 498-516 PR00887B 9.94 3.250e-22 365-382 PR00887C 13.16 4.000e-22 388-405 PR00887E 10.36 5.200e-22 480-499 PR00887H 11.84 8.313e-22 537-556 PR00887G 14.17 9.438e-20 521-538 PR00887D 15.12 8.313e-17 453-467
1090	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE	PR00886C 11.84 8.500e-13 696-715 PR00886A 10.08 3.192e-10 710-733
1090	PD02448	TRANSCRIPTION PROTEIN DNA-BINDIN.	PD02448A 9.37 5.576e-10 686-725
1090	BL00353	HMG1/2 proteins.	BL00353B 11.47 8.244e-24 664-714 BL00353A 9.60 2.549e-09 674-723
1091	BL00284	Serpins proteins.	BL00284C 28.56 4.000e-25 472-514 BL00284D 16.34 5.655e-17 578-605 BL00284A 15.64 2.742e-15 341-365 BL00284E 19.15 4.818e-15 659-684 BL00284B 17.99 3.667e-14 445-466 BL00284A 15.64 2.600e-11 375-399
1092	PR00839	V8 SERINE PROTEASE FAMILY SIGNATURE	PR00839B 11.20 8.119e-10 357-375
1097	BL00605	ATP synthase c subunit proteins.	BL00605 27.67 3.172e-33 79-133
1097	PR00124	ATP SYNTHASE C SUBUNIT SIGNATURE	PR00124C 12.42 6.400e-18 113-139 PR00124A 8.81 8.054e-14 75-95 PR00124B 14.66 6.897e-12 96-112
1098	BL00450	Aconitase family proteins.	BL00450B 42.34 8.393e-30 386-441 BL00450D 21.14 2.800e-18 665-689 BL00450E 16.34 8.875e-13 710-725 BL00450B 42.34

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SEQ ID	Database entry ID	Description	Results*
			6.400e-12 446-501 BL00450A 13.76 2.406e-11 351-365 BL00450C 11.95 6.657e-10 612-622
1098	PR00415	ACONITASE FAMILY SIGNATURE	PR00415D 12.72 5.696e-16 390-406 PR00415I 13.62 4.115e-15 675-689 PR00415G 14.24 8.105e-15 548-563 PR00415C 13.34 7.828e-14 376-390 PR00415E 10.04 7.828e-14 452-466 PR00415F 11.66 7.273e-13 466-480 PR00415H 12.39 9.700e-13 613-625 PR00415A 11.15 1.621e-10 323-337 PR00415B 8.14 9.036e-09 347-356
1104	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 1.000e-11 139-149
1104	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 4.255e-09 85-109
1106	BL01002	Translationally controlled tumor protein.	BL01002C 21.97 6.143e-26 79-110 BL01002A 13.19 1.360e-24 1-24 BL01002B 7.39 3.118e-14 48-62
1107	PF00997	Kappa casein.	PF00997D 9.95 8.306e-09 513-548
1109	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 1.391e-09 42-55
1110	BL01310	ATP1G1 / PLM / MAT8 family proteins.	BL01310 14.74 8.981e-24 99-135
1112	PR00764	COMPLEMENT C9 SIGNATURE	PR00764B 13.56 2.250e-11 122-143
1112	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE	PR00261E 11.08 6.308e-09 127-149 PR00261F 11.57 7.152e-09 127-149
1115	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 4.273e-14 188-228
1115	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245A 18.03 3.250e-19 157-179 PR00245B 10.38 1.918e-09 275-290
1115	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237C 15.69 4.150e-09 202-225
1116	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 2.658e-12 163-203
1116	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245A 18.03 9.325e-19 132-154 PR00245C 7.84 4.073e-15 311-327 PR00245B 10.38 5.500e-13 250-265 PR00245E 12.40 7.618e-13 364-379 PR00245D 10.47 4.673e-09 347-359
1116	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237C 15.69 6.400e-10 177-200 PR00237G 19.63 5.814e-09 345-372
1119	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 7.955e-13 969-997 PD01719A 12.89 8.111e-09 305-333
1120	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 1.692e-37 18-49
1120	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY	PR00925A 5.47 2.800e-19 18-33 PR00925B 3.73 3.400e-16 34-47

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SEQ ID	Database entry ID	Description	Results*
		SIGNATURE	PR00925D 6.56 2.200e-13 66-77 PR00925C 5.57 8.235e-09 47-58
1124	BL00615	C-type lectin domain proteins.	BL00615A 16.68 4.240e-11 210-228
1125	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327B 19.84 2.091e-09 191-213
1125	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 7.652e-09 338-348
1127	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870D 15.74 8.755e-09 96-131
1133	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245A 18.03 8.364e-14 122-144 PR00245C 7.84 9.280e-13 300-316 PR00245B 10.38 4.600e-11 240-255 PR00245E 12.40 7.623e-10 353-368
1133	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 5.371e-13 153-193 BL00237D 11.23 7.750e-10 344-361
1133	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237G 19.63 6.063e-12 334-361 PR00237C 15.69 6.175e-09 167-190
1134	BL00221	MIP family proteins.	BL00221B 10.22 1.871e-11 141-152 BL00221D 12.33 2.174e-11 240-255 BL00221E 8.47 9.710e-11 307-318 BL00221A 6.39 5.935e-09 92-103
1134	PR00783	MAJOR INTRINSIC PROTEIN FAMILY SIGNATURE	PR00783B 15.98 4.130e-15 127-152 PR00783F 12.33 9.156e-14 308-329 PR00783A 12.72 7.462e-12 88-108 PR00783E 16.78 8.263e-10 128-151 PR00783C 13.54 1.340e-09 164-184 PR00783E 16.78 6.754e-09 226-249
1136	PD02886	GLYCOPROTEIN PRECURSOR IMMUNOGLOBULIN FOL.	PD02886C 21.92 7.907e-10 112-151
1137	PR00122	VACUOLAR ATP SYNTHASE 16 KD SUBUNIT SIGNATURE	PR00122C 8.20 1.000e-33 104-131 PR00122B 8.60 2.125e-28 56-81 PR00122D 9.97 4.375e-28 131-155 PR00122A 11.44 6.053e-19 30-55
1137	BL00605	ATP synthase c subunit proteins.	BL00605 27.67 1.778e-10 94-148
1137	PR00124	ATP SYNTHASE C SUBUNIT SIGNATURE	PR00124C 12.42 2.161e-10 128-154
1138	BL00665	Dihydrodipicolinate synthetase proteins.	BL00665B 30.33 8.265e-12 52-105 BL00665D 14.76 1.000e-11 164-187 BL00665C 25.58 5.832e-11 105-156
1138	PR00146	DIHYDRODIPICOLINATE SYNTHASE SIGNATURE	PR00146D 16.26 2.525e-10 163-181
1139	BL00456	Sodium:solute symporter family proteins.	BL00456C 24.55 4.886e-28 165-220 BL00456A 22.59 3.127e-27 27-82 BL00456B 18.94 1.220e-17 103-133
1139	BL00415	Synapsins proteins.	BL00415O 3.44 6.270e-09 514-552
1139	BL00136	Serine proteases, subtilase family, aspartic acid proteins.	BL00136B 9.63 7.796e-09 773-786

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SEQ ID	Database entry ID	Description	Results*
1141	BL00310	Lysosome-associated membrane glycoproteins duplicated domain proteins.	BL00310F 23.26 4.162e-09 194-249
1143	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 4.115e-18 126-166 BL00237C 13.19 7.545e-15 263-290 BL00237D 11.23 8.962e-11 324-341
1143	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237G 19.63 7.120e-15 314-341 PR00237F 13.57 2.565e-14 268-293 PR00237C 15.69 6.667e-12 140-163 PR00237A 11.48 8.125e-11 63-88 PR00237B 13.50 1.563e-10 96-118 PR00237E 13.03 3.118e-09 226-250
1144	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 2.068e-09 7-22
1145	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 1.310e-14 387-402
1145	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 6.906e-15 387-402 PR00403A 16.82 5.200e-11 373-387
1145	BL01179	Phosphotyrosine interaction domain proteins (PID) profile.	BL01179A 12.63 8.286e-11 394-406 BL01179B 15.18 7.968e-10 667-682
1147	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 3.851e-09 107-151
1148	PR00399	SYNAPTOTAGMIN SIGNATURE	PR00399B 14.27 1.305e-09 242-256
1148	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 6.318e-09 279-293
1150	BL00291	Prion protein.	BL00291A 4.49 8.241e-09 21-56
1152	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 6.447e-12 210-250
1152	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237G 19.63 3.512e-09 392-419 PR00237C 15.69 4.825e-09 224-247
1152	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245A 18.03 1.500e-20 179-201 PR00245B 10.38 3.571e-16 297-312 PR00245E 12.40 1.000e-12 411-426 PR00245D 10.47 1.000e-10 394-406 PR00245C 7.84 6.727e-09 358-374
1153	PR00962	LETHAL(2) GIANT LARVAE PROTEIN SIGNATURE	PR00962B 11.98 2.800e-28 310-333 PR00962G 15.71 5.655e-28 609-634 PR00962D 10.40 1.225e-27 451-475 PR00962F 12.39 6.786e-23 568-588 PR00962H 13.32 9.710e-23 639-659 PR00962I 11.68 3.829e-22 708-728 PR00962C 8.00 4.250e-22 362-383 PR00962A 13.28 7.612e-22 17-36 PR00962E 8.81 1.628e-20 531-550
1153	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 9.122e-09 454-469
1155	BL00218	Amino acid permeases proteins.	BL00218D 21.49 2.038e-10 385-430 BL00218E 23.30 6.400e-10 466-506 BL00218B 21.44 5.790e-

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SEQ ID	Database entry ID	Description	Results*
			09 217-249
1155	BL00341	Surfactant associated polypeptide SP-C palmitoylation site proteins.	BL00341B 8.70 7.895e-09 54-88
1158	PR00783	MAJOR INTRINSIC PROTEIN FAMILY SIGNATURE	PR00783C 13.54 1.474e-17 31-51
1158	BL00221	MIP family proteins.	BL00221B 10.22 1.643e-14 8-19
1158	PD00302	PROTEASE POLYPROTEIN HYDROLASE ASP.	PD00302B 9.52 1.360e-14 261-277 PD00302A 6.33 3.323e-11 198-209
1158	PF00692	dUTPase.	PF00692B 8.14 3.613e-11 113-124
1158	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.818e-13 292-326 DM00892B 9.78 1.000e-08 264-270
1160	PD00320	LAMININ CHAIN EGF-LIKE DOMAIN P.	PD00320A 14.49 8.286e-12 1681-1695
1160	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 1.225e-09 1745-1761
1160	BL01248	Laminin-type EGF-like (LE) domain proteins.	BL01248 11.02 9.308e-18 1705-1718 BL01248 11.02 4.000e-15 393-406 BL01248 11.02 1.900e-11 321-334 BL01248 11.02 6.094e-09 445-458
1160	PR00877	PLANT PEC FAMILY METALLOTHIONEIN SIGNATURE	PR00877D 4.18 6.516e-09 1308-1316
1160	PF00054	Laminin G domain proteins.	PF00054B 16.61 8.200e-09 558-570
1160	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 2.841e-17 547-566 PR00011D 14.03 4.150e-16 547-566 PR00011B 13.08 7.750e-16 1370-1389 PR00011A 14.06 1.170e-15 1277-1296 PR00011D 14.03 4.000e-15 501-520 PR00011A 14.06 4.736e-15 547-566 PR00011A 14.06 1.327e-14 1370-1389 PR00011A 14.06 5.909e-14 1416-1435 PR00011D 14.03 7.980e-14 1370-1389 PR00011D 14.03 3.717e-13 1416-1435 PR00011D 14.03 6.434e-13 1277-1296 PR00011B 13.08 8.932e-13 1277-1296 PR00011A 14.06 2.161e-12 436-455 PR00011D 14.03 6.053e-12 436-455 PR00011B 13.08 1.138e-11 436-455 PR00011B 13.08 6.954e-11 1416-1435 PR00011A 14.06 8.062e-11 1318-1337 PR00011A 14.06 1.913e-10 695-714 PR00011B 13.08 2.043e-10 644-663 PR00011D 14.03 3.215e-10 695-714 PR00011C 24.25 4.600e-10 651-680 PR00011C 24.25 9.100e-10 1423-1452 PR00011D 14.03 1.261e-09 644-663 PR00011B 13.08 1.370e-09 695-714 PR00011A 14.06 1.986e-09 644-663 PR00011B 13.08 3.096e-

Table 3A
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SEQ ID	Database entry ID	Description	Results*
			09 1318-1337 PR00011D 14.03 8.435e-09 591-610 PR00011C 24.25 9.857e-09 1769-1798
1161	PD00919	CALCIUM-BINDING PRECURSOR SIGNAL R.	PD00919A 11.53 8.377e-10 185-197
1161	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 9.486e-10 158-174 BL01187B 12.04 2.800e-09 196-212
1161	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 4.158e-12 39-58 PR00011B 13.08 2.973e-09 39-58
1161	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 5.929e-09 163-174
1161	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243H 17.53 7.276e-09 65-91
1161	BL01185	C-terminal cystine knot proteins.	BL01185B 21.14 9.047e-09 137-186
1161	DM00060	338 kw NEUREXIN ALPHA III CYSTEINE.	DM00060 6.92 9.460e-09 108-118
1161	BL01248	Laminin-type EGF-like (LE) domain proteins.	BL01248 11.02 9.660e-09 48-61
1162	BL00252	Interferon alpha, beta and delta family proteins.	BL00252A 18.49 6.657e-23 35-72 BL00252B 19.78 9.125e-16 73-124
1162	PR00266	INTERFERON ALPHA AND BETA SUBUNIT SIGNATURE	PR00266A 13.61 1.000e-13 67-80
1163	PR00264	INTERLEUKIN-1 SIGNATURE	PR00264B 20.98 8.453e-11 63-90 PR00264C 17.77 1.851e-10 103-132
1164	BL00249	Platelet-derived growth factor (PDGF) family proteins.	BL00249 18.21 3.250e-34 75-105
1165	BL00253	Interleukin-1 proteins.	BL00253D 25.67 3.464e-11 95-135
1165	PR00264	INTERLEUKIN-1 SIGNATURE	PR00264C 17.77 3.294e-17 95-124 PR00264B 20.98 6.250e-09 56-83
1166	PR00573	INTERLEUKIN 8B RECEPTOR SIGNATURE	PR00573D 15.57 1.450e-20 114-130
1166	PR00427	INTERLEUKIN-8 RECEPTOR SIGNATURE	PR00427E 7.08 9.446e-18 6-22 PR00427G 10.85 2.667e-16 98-115 PR00427F 11.77 9.500e-13 48-65
1166	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237F 13.57 4.789e-16 23-48 PR00237G 19.63 1.844e-12 70-97
1166	BL00237	G-protein coupled receptors proteins.	BL00237C 13.19 1.857e-16 18-45 BL00237D 11.23 6.464e-10 80-97
1167	PR00414	PALMITOYL PROTEIN THIOESTERASE SIGNATURE	PR00414A 10.74 1.000e-31 26-49 PR00414D 17.19 1.450e-27 151-171 PR00414E 16.76 1.600e-27 185-205 PR00414G 12.38 4.000e-25 258-277 PR00414B 12.48 4.214e-25 66-86 PR00414C 13.14 1.000e-22 106-123
1168	BL00284	Serpins proteins.	BL00284C 28.56 4.000e-25 204-246 BL00284A 15.64 7.750e-22 73-97 BL00284E 19.15 8.826e-19 391-416 BL00284D 16.34 5.655e-17 310-337 BL00284B 17.99 3.667e-14 177-198 BL00284A 15.64 2.600e-11 107-131
1170	BL00269	Mammalian defensins proteins.	BL00269C 16.52 6.786e-26 103-

Table 3A
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SEQ ID	Database entry ID	Description	Results*
			132 BL00269A 8.53 2.607e-20 38-58 BL00269B 19.17 5.500e-17 65-94
1172	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383A 13.34 5.235e-16 274-289 BL00383F 15.51 1.429e-15 477-493 BL00383E 10.35 7.000e-15 439-450 BL00383D 11.92 4.000e-13 403-416 BL00383C 10.10 6.344e-10 326-337
1172	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 5.320e-21 313-334 PR00700D 12.47 9.217e-19 436-455 PR00700C 13.17 3.143e-15 399-417 PR00700F 11.18 8.941e-13 483-494 PR00700A 6.96 8.714e-10 295-303 PR00700E 17.57 7.618e-09 467-483
1174	BL00472	Small cytokines (intercrine/chemokine) C-C subfamily signatur.	BL00472A 7.45 3.483e-09 1-13
1175	BL00472	Small cytokines (intercrine/chemokine) C-C subfamily signatur.	BL00472A 7.45 3.483e-09 1-13
1187	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 4.273e-09 88-102
1188	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860B 7.04 6.776e-09 52-66
1189	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 1.514e-30 276-320 BL00280 24.61 6.553e-24 238-282
1189	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE	PR00759C 14.15 2.385e-14 304-320 PR00759B 11.26 8.105e-12 256-267 PR00759B 11.26 2.452e-10 294-305
1189	BL00213	Lipocalin proteins.	BL00213A 12.95 2.636e-09 38-52
1189	PR00179	LIPOCALIN SIGNATURE	PR00179B 9.56 8.125e-12 122-135 PR00179A 13.78 6.760e-10 38-51 PR00179C 19.02 6.727e-09 150-166
1190	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 1.000e-10 83-117
1191	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 1.000e-10 83-117
1198	BL00154	E1-E2 ATPases phosphorylation site proteins.	BL00154G 21.18 9.783e-09 203-237
1200	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 3.494e-09 120-133
1201	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.500e-28 35-74
1202	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.500e-28 35-74
1204	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 7.158e-19 81-98
1204	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722A 12.27 7.353e-18 82-98
1204	BL00495	Apple domain proteins.	BL00495K 12.58 4.543e-11 83-116
1204	BL01253	Type I fibronectin domain proteins.	BL01253E 16.01 3.415e-13 154-191 BL01253D 4.84 9.585e-11 81-95
1204	BL00021	Kringle domain proteins.	BL00021B 13.33 2.370e-17 81-99

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SEQ ID	Database entry ID	Description	Results*
			BL00021C 22.21 6.604e-09 165-187
1208	PR00179	LIPOCALIN SIGNATURE	PR00179B 9.56 7.214e-09 121-134
1212	PR00364	DISEASE RESISTANCE PROTEIN SIGNATURE	PR00364D 10.54 6.700e-09 172-189
1212	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 8.615e-13 177-191 PR00019B 11.36 2.286e-12 174-188 PR00019A 11.19 4.913e-10 319-333 PR00019B 11.36 4.960e-09 387-401 PR00019A 11.19 8.667e-09 151-165
1213	BL00132	Zinc carboxypeptidases, zinc-binding region 1 proteins.	BL00132C 21.35 3.308e-28 129-170 BL00132B 15.93 1.871e-16 99-113 BL00132A 26.07 1.682e-14 50-91 BL00132F 13.26 7.254e-14 228-250 BL00132D 12.70 2.875e-12 173-188 BL00132E 17.72 3.552e-12 199-226
1213	PR00765	CARBOXYPEPTIDASE A METALLOPROTEASE (M14) FAMILY SIGNATURE	PR00765B 15.57 7.857e-16 99-114 PR00765D 14.16 5.500e-11 233-247 PR00765C 12.55 1.290e-10 179-188
1214	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270C 19.54 5.329e-09 32-61
1221	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007A 19.33 1.000e-16 143-170 PR00007C 15.60 8.200e-15 214-236 PR00007B 14.16 5.846e-14 170-190 PR00007D 9.64 5.250e-10 249-260
1221	BL01113	C1q domain proteins.	BL01113B 18.26 1.581e-29 149-185 BL01113C 13.18 3.077e-15 214-234 BL01113A 17.99 1.243e-13 50-77 BL01113A 17.99 6.108e-13 35-62 BL01113A 17.99 3.077e-12 41-68 BL01113A 17.99 1.574e-10 38-65 BL01113A 17.99 9.617e-10 44-71 BL01113A 17.99 7.577e-09 59-86
1221	BL00420	Speract receptor repeat proteins domain proteins.	BL00420A 20.42 2.038e-12 86-115 BL00420A 20.42 5.154e-12 44-73 BL00420A 20.42 4.185e-09 47-76 BL00420A 20.42 9.031e-09 50-79
1223	BL00240	Receptor tyrosine kinase class III proteins.	BL00240E 11.56 2.043e-21 260-298 BL00240F 17.74 4.035e-18 313-361 BL00240G 28.45 4.923e-17 361-414
1223	BL50001	Src homology 2 (SH2) domain proteins profile.	BL50001B 17.40 3.077e-16 271-292
1223	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.500e-19 274-305 BL00107B 13.31 7.231e-12 342-358
1223	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 4.462e-20 343-366 PR00109E 14.41 5.950e-20 388-411 PR00109B 12.27 9.571e-19 274-293 PR00109A 15.00 5.065e-10 237-251 PR00109C

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SEQ ID	Database entry ID	Description	Results*
			12.85 5.333e-10 324-335
1223	BL00239	Receptor tyrosine kinase class II proteins.	BL00239E 17.14 1.281e-25 314-364 BL00239F 28.15 9.684e-19 369-414 BL00239C 18.75 8.765e-15 261-284 BL00239D 16.81 5.571e-10 286-312
1223	PR00046	MAJOR SIGMA-70 FACTOR SIGNATURE	PR00046A 13.26 8.788e-09 296-310
1223	BL00790	Receptor tyrosine kinase class V proteins.	BL00790O 7.68 9.357e-16 321-354 BL00790Q 15.61 6.057e-11 380-429 BL00790N 13.25 3.937e-10 287-314 BL00790M 8.74 5.138e-10 265-287 BL00790K 9.30 1.000e-08 182-236
1224	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE	PR00453A 12.79 9.827e-09 50-68
1227	BL00615	C-type lectin domain proteins.	BL00615B 12.25 9.571e-10 151-165 BL00615A 16.68 3.100e-09 48-66
1237	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514E 14.28 7.750e-12 313-330
1257	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 1.000e-09 247-261 PR00019B 11.36 2.080e-09 316-330 PR00019B 11.36 3.160e-09 244-258 PR00019B 11.36 4.240e-09 100-114 PR00019B 11.36 5.680e-09 148-162
1263	BL00427	Disintegrins proteins.	BL00427 13.93 4.035e-17 436-491
1263	PR00289	DISINTEGRIN SIGNATURE	PR00289A 13.62 5.667e-14 450-470
1263	PR00873	ECHINOIDEA (SEA URCHIN) METALLOTHIONEIN SIGNATURE	PR00873D 8.43 5.989e-09 608-627
1264	BL01173	Lipolytic enzymes G-D-X-G family, histidine.	BL01173C 8.98 1.000e-16 216-230 BL01173B 13.27 1.000e-12 174-201 BL01173A 9.41 7.200e-11 141-154
1266	BL00492	Clusterin proteins.	BL00492F 16.61 1.000e-40 163-205 BL00492G 13.20 1.000e-40 230-280 BL00492H 16.50 6.870e-40 358-395 BL00492C 8.35 1.000e-38 52-86 BL00492B 10.36 9.053e-28 26-49 BL00492E 12.52 6.423e-26 73-122 BL00492A 11.53 4.724e-18 2-19
1267	BL00284	Serpins proteins.	BL00284C 28.56 6.538e-29 207-249 BL00284A 15.64 3.739e-18 107-131 BL00284D 16.34 3.793e-17 314-341 BL00284E 19.15 2.909e-15 401-426
1268	BL00284	Serpins proteins.	BL00284C 28.56 6.538e-29 243-285 BL00284A 15.64 3.739e-18 125-149 BL00284E 19.15 8.269e-18 437-462 BL00284D 16.34 3.793e-17 350-377 BL00284B 17.99 3.483e-13 214-235
1273	BL00380	Rhodanese proteins.	BL00380D 15.90 8.200e-28 110-

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SEQ ID	Database entry ID	Description	Results*
			136 BL00380G 11.26 5.800e-16 251-264 BL00380B 14.77 7.000e-14 49-62 BL00380C 15.67 7.387e-13 82-98 BL00380E 12.44 7.000e-11 181-193 BL00380A 10.48 1.000e-09 10-20
1274	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134C 13.45 9.000e-17 333-347 BL00134A 11.96 7.429e-16 147-164 BL00134B 15.99 3.793e-15 297-321
1274	BL01253	Type I fibronectin domain proteins.	BL01253H 13.15 5.909e-19 315-350 BL01253G 11.34 8.791e-13 296-310 BL01253F 14.35 2.241e-12 252-291 BL01253E 16.01 7.194e-10 215-252 BL01253D 4.84 7.686e-10 147-161
1274	BL00495	Apple domain proteins.	BL00495N 11.04 3.957e-24 289-324 BL00495O 13.75 6.610e-16 324-353 BL00495K 12.58 1.957e-11 149-182 BL00495L 11.94 2.154e-09 178-217
1274	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722A 12.27 7.480e-15 148-164 PR00722C 10.87 2.286e-14 296-309 PR00722B 12.51 3.250e-09 203-218
1274	BL00021	Kringle domain proteins.	BL00021D 24.56 8.773e-27 305-347 BL00021B 13.33 9.217e-17 147-165 BL00021C 22.21 3.717e-09 226-248
1279	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	PR00704I 9.52 4.682e-14 145-174
1287	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.313e-28 16-55
1287	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.769e-15 191-204 PD00066 13.92 1.500e-13 247-260 PD00066 13.92 1.500e-13 387-400 PD00066 13.92 7.500e-13 275-288 PD00066 13.92 8.000e-13 359-372 PD00066 13.92 9.143e-12 219-232 PD00066 13.92 4.913e-11 303-316
1287	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.857e-16 371-388 BL00028 16.07 8.412e-14 203-220 BL00028 16.07 5.500e-13 287-304 BL00028 16.07 1.346e-11 259-276 BL00028 16.07 5.154e-11 399-416 BL00028 16.07 7.577e-11 343-360 BL00028 16.07 1.000e-10 175-192 BL00028 16.07 6.700e-10 231-248 BL00028 16.07 3.829e-09 315-332
1287	PD02462	PROTEIN BOLA TRANSCRIPTION REGULATION AC.	PD02462A 22.48 6.817e-09 280-315
1287	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.750e-16 368-382 PR00048A 10.52 4.273e-15 284-298 PR00048A 10.52 1.643e-13 200-214 PR00048B 6.02 1.900e-13 188-198 PR00048B 6.02

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SEQ ID	Database entry ID	Description	Results*
			6.400e-13 272-282 PR00048A 10.52 3.118e-12 396-410 PR00048B 6.02 5.000e-12 384-394 PR00048B 6.02 4.462e-11 244-254 PR00048B 6.02 1.563e-10 356-366 PR00048A 10.52 2.174e-10 256-270 PR00048A 10.52 4.913e-10 312-326 PR00048A 10.52 9.217e-10 340-354 PR00048B 6.02 3.368e-09 300-310 PR00048A 10.52 7.480e-09 228-242
1292	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243H 17.53 8.696e-11 42-68
1295	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.512e-31 10-49
1295	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.100e-16 337-350 PD00066 13.92 4.462e-15 477-490 PD00066 13.92 5.800e-14 421-434 PD00066 13.92 9.400e-14 449-462 PD00066 13.92 9.500e-13 365-378 PD00066 13.92 9.500e-13 393-406
1295	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.353e-14 321-338 BL00028 16.07 7.750e-13 405-422 BL00028 16.07 9.550e-13 349-366 BL00028 16.07 9.550e-13 377-394 BL00028 16.07 2.957e-12 433-450 BL00028 16.07 5.800e-10 461-478 BL00028 16.07 7.600e-10 489-506
1295	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-13 346-360 PR00048A 10.52 1.000e-13 486-500 PR00048A 10.52 5.500e-13 430-444 PR00048A 10.52 6.786e-13 402-416 PR00048A 10.52 6.786e-13 458-472 PR00048A 10.52 4.789e-11 318-332 PR00048A 10.52 9.526e-11 374-388 PR00048B 6.02 1.000e-10 334-344 PR00048B 6.02 9.438e-10 418-428 PR00048B 6.02 9.438e-10 474-484 PR00048B 6.02 8.579e-09 446-456
1296	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.615e-33 16-55
1296	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.400e-16 348-361 PD00066 13.92 3.077e-15 236-249 PD00066 13.92 4.462e-15 264-277 PD00066 13.92 4.462e-15 320-333 PD00066 13.92 2.800e-14 432-445 PD00066 13.92 4.600e-14 292-305 PD00066 13.92 8.200e-14 488-501 PD00066 13.92 8.200e-14 516-529 PD00066 13.92 6.500e-13 376-389 PD00066 13.92 7.000e-13 208-221 PD00066 13.92 4.429e-12 460-473
1296	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 9.182e-15 385-399 PR00048A 10.52 9.182e-15

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SEQ ID	Database entry ID	Description	Results*
			469-483 PR00048A 10.52 4.750e-14 329-343 PR00048A 10.52 3.571e-13 413-427 PR00048A 10.52 9.357e-13 245-259 PR00048A 10.52 1.529e-12 525-539 PR00048A 10.52 2.588e-12 189-203 PR00048A 10.52 3.118e-12 301-315 PR00048A 10.52 3.647e-12 357-371 PR00048B 6.02 1.000e-11 205-215 PR00048B 6.02 1.000e-11 261-271 PR00048B 6.02 1.000e-11 429-439 PR00048B 6.02 2.385e-11 345-355 PR00048B 6.02 4.462e-11 513-523 PR00048B 6.02 7.231e-11 317-327 PR00048A 10.52 9.526e-11 217-231 PR00048A 10.52 2.174e-10 273-287 PR00048B 6.02 2.688e-10 485-495 PR00048B 6.02 3.813e-10 289-299 PR00048B 6.02 4.938e-10 233-243 PR00048A 10.52 6.478e-10 497-511 PR00048B 6.02 3.842e-09 373-383
1296	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.588e-14 192-209 BL00028 16.07 1.450e-13 388-405 BL00028 16.07 1.450e-13 528-545 BL00028 16.07 5.304e-12 472-489 BL00028 16.07 6.478e-12 416-433 BL00028 16.07 8.826e-12 332-349 BL00028 16.07 9.609e-12 248-265 BL00028 16.07 2.385e-11 276-293 BL00028 16.07 3.769e-11 360-377 BL00028 16.07 7.577e-11 304-321 BL00028 16.07 6.100e-10 220-237 BL00028 16.07 5.886e-09 500-517
1299	BL00142	Neutral zinc metallopeptidases, zinc-binding region proteins.	BL00142 8.38 4.375e-10 188-199
1299	PR00138	MATRIXIN SIGNATURE	PR00138D 16.56 1.321e-19 188-214 PR00138B 15.82 1.655e-10 106-122 PR00138C 16.41 2.393e-10 132-161 PR00138E 6.01 6.586e-10 222-236
1299	BL00024	Hemopexin domain proteins.	BL00024D 17.28 3.411e-22 182-214 BL00024B 21.53 8.788e-19 80-114 BL00024H 11.35 3.077e-10 337-349 BL00024E 7.58 9.211e-10 222-236 BL00024C 22.98 6.000e-09 131-180
1299	PR00480	ASTACIN FAMILY SIGNATURE	PR00480B 15.41 6.529e-09 183-202
1299	BL00546	Matrixins cysteine switch.	BL00546C 16.41 1.643e-22 182-214 BL00546D 10.34 8.017e-10 222-236 BL00546B 20.11 2.443e-09 132-176 BL00546H 10.76 4.512e-09 337-348 BL00546G 16.84 6.684e-09 338-358

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SEQ ID	Database entry ID	Description	Results*
1301	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.875e-09 170-188
1305	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e-22 60-98 PD02811B 17.07 2.263e-21 111-144 PD02811C 13.25 5.696e-13 147-160
1307	BL00282	Kazal serine protease inhibitors family proteins.	BL00282 16.88 8.043e-18 28-51
1307	PR00290	KAZAL-TYPE SERINE PROTEASE INHIBITOR SIGNATURE	PR00290B 9.78 6.559e-11 39-51 PR00290A 10.88 8.851e-09 28-39
1308	BL00112	ATP:guanido phosphotransferases proteins.	BL00112F 21.37 7.728e-09 51-102
1309	BL00269	Mammalian defensins proteins.	BL00269C 16.52 6.786e-26 139-168 BL00269A 8.53 2.607e-20 74-94 BL00269B 19.17 5.500e-17 101-130
1312	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.559e-12 63-107
1312	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.545e-17 63-85 PR00449E 13.50 9.280e-14 201-224 PR00449D 10.79 7.158e-13 167-181 PR00449C 17.27 9.229e-12 103-126 PR00449B 14.34 9.280e-10 86-103
1314	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.059e-14 361-378 BL00028 16.07 7.353e-14 193-210 BL00028 16.07 1.900e-13 165-182 BL00028 16.07 3.250e-13 333-350 BL00028 16.07 4.150e-13 221-238 BL00028 16.07 9.550e-13 277-294 BL00028 16.07 1.000e-11 305-322 BL00028 16.07 1.600e-10 249-266
1314	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.800e-14 321-334 PD00066 13.92 1.000e-13 265-278 PD00066 13.92 1.429e-12 237-250 PD00066 13.92 7.857e-12 181-194 PD00066 13.92 2.174e-11 349-362 PD00066 13.92 2.385e-10 209-222 PD00066 13.92 7.231e-10 293-306
1314	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.500e-14 218-232 PR00048A 10.52 5.500e-14 358-372 PR00048A 10.52 8.500e-14 330-344 PR00048A 10.52 2.286e-13 190-204 PR00048A 10.52 8.071e-13 162-176 PR00048A 10.52 3.118e-12 274-288 PR00048A 10.52 6.684e-11 246-260 PR00048B 6.02 7.231e-11 318-328 PR00048B 6.02 1.563e-10 178-188 PR00048A 10.52 7.261e-10 302-316 PR00048B 6.02 8.579e-09 262-272
1315	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 1.947e-10 95-123
1315	PR00874	FUNGI-IV METALLOTHIONEIN SIGNATURE	PR00874C 4.37 3.750e-09 48-63

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SEQ ID	Database entry ID	Description	Results*
1315	BL00269	Mammalian defensins proteins.	BL00269C 16.52 4.434e-09 50-79
1315	PD00866	GLYCOPROTEIN PROTEIN SPIKE E2 PRECURSOR PEPLIMER.	PD00866L 3.73 2.770e-09 24-34 PD00866L 3.73 2.770e-09 82-92 PD00866L 3.73 2.918e-09 4-14 PD00866L 3.73 4.984e-09 14-24
1315	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 5.014e-09 89-103
1315	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 5.655e-13 3-46 BL00243I 31.77 9.286e-11 81-124 BL00243I 31.77 6.691e-10 13-56 BL00243I 31.77 2.775e-09 10-53 BL00243I 31.77 5.310e-09 52-95 BL00243I 31.77 5.437e-09 18-61
1315	PR00858	CRUSTACEAN METALLOTHIONEIN SIGNATURE	PR00858B 5.93 3.394e-09 49-68 PR00858B 5.93 7.223e-09 15-34
1315	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 9.893e-13 72-118 BL00203 13.94 7.414e-12 34-80 BL00203 13.94 2.879e-11 46-92 BL00203 13.94 4.956e-11 87-133 BL00203 13.94 5.945e-11 101-147 BL00203 13.94 8.319e-11 78-124 BL00203 13.94 1.383e-10 63-109 BL00203 13.94 3.106e-10 77-123 BL00203 13.94 6.266e-10 15-61 BL00203 13.94 8.085e-10 33-79 BL00203 13.94 8.372e-10 102-148 BL00203 13.94 9.138e-10 56-102 BL00203 13.94 9.521e-10 88-134 BL00203 13.94 1.000e-09 5-51 BL00203 13.94 1.827e-09 82-128 BL00203 13.94 3.847e-09 83-129 BL00203 13.94 5.133e-09 48-94 BL00203 13.94 5.500e-09 25-71 BL00203 13.94 6.143e-09 28-74 BL00203 13.94 6.327e-09 93-139 BL00203 13.94 7.337e-09 73-119 BL00203 13.94 8.071e-09 61-107 BL00203 13.94 8.439e-09 91-137 BL00203 13.94 9.082e-09 13-59
1315	DM00864	EGF-LIKE DOMAIN.	DM00864A 15.21 9.229e-09 6-27
1315	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 1.600e-09 23-35 BL00198 10.43 9.700e-09 3-15
1316	DM00406	GLIADIN.	DM00406 7.73 9.514e-10 162-175
1316	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 8.859e-09 66-109
1316	BL00269	Mammalian defensins proteins.	BL00269C 16.52 4.553e-09 24-53 BL00269C 16.52 9.289e-09 94-123
1316	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 3.700e-09 45-73 PD02283C 17.54 8.763e-09 65-93 PD02283C 17.54 9.325e-09 80-108 PD02283C 17.54 9.550e-09 90-118
1316	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 4.363e-11 47-93 BL00203 13.94 5.846e-11 88-134 BL00203 13.94 7.527e-11 57-103 BL00203 13.94 8.714e-11 22-68 BL00203 13.94 4.447e-10 87-133

Table 3A
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SEQ ID	Database entry ID	Description	Results*
			BL00203 13.94 7.798e-10 92-138 BL00203 13.94 2.010e-09 37-83 BL00203 13.94 3.939e-09 38-84 BL00203 13.94 5.133e-09 18-64 BL00203 13.94 5.224e-09 17-63 BL00203 13.94 5.592e-09 52-98 BL00203 13.94 5.684e-09 68-114 BL00203 13.94 7.153e-09 33-79 BL00203 13.94 7.245e-09 78-124 BL00203 13.94 8.163e-09 43-89 BL00203 13.94 8.439e-09 23-69 BL00203 13.94 9.265e-09 42-88 BL00203 13.94 9.633e-09 93-139
1317	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 8.279e-10 216-259 BL00243I 31.77 5.310e-09 219-262
1317	BL01208	VWFC domain proteins.	BL01208B 15.83 5.865e-09 244-259
1317	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 7.750e-10 163-191 PD02283C 17.54 4.938e-09 198-226 PD02283C 17.54 6.175e-09 243-271 PD02283C 17.54 6.400e-09 62-90 PD02283C 17.54 6.625e-09 153-181 PD02283C 17.54 6.738e-09 173-201 PD02283C 17.54 6.738e-09 208-236 PD02283C 17.54 7.975e-09 188-216 PD02283C 17.54 9.325e-09 178-206
1317	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 9.703e-11 130-176 BL00203 13.94 1.191e-10 104-150 BL00203 13.94 2.149e-10 64-110 BL00203 13.94 4.447e-10 200-246 BL00203 13.94 5.883e-10 215-261 BL00203 13.94 5.979e-10 210-256 BL00203 13.94 5.979e-10 225-271 BL00203 13.94 6.362e-10 120-166 BL00203 13.94 6.649e-10 24-70 BL00203 13.94 7.032e-10 34-80 BL00203 13.94 8.181e-10 165-211 BL00203 13.94 8.947e-10 85-131 BL00203 13.94 9.809e-10 60-106 BL00203 13.94 1.000e-09 170-216 BL00203 13.94 1.367e-09 176-222 BL00203 13.94 1.643e-09 70-116 BL00203 13.94 2.378e-09 239-285 BL00203 13.94 2.469e-09 125-171 BL00203 13.94 3.755e-09 175-221 BL00203 13.94 3.847e-09 19-65 BL00203 13.94 3.847e-09 190-236 BL00203 13.94 4.122e-09 201-247 BL00203 13.94 4.490e-09 160-206 BL00203 13.94 5.224e-09 186-232 BL00203 13.94 5.867e-09 115-161 BL00203 13.94 6.235e-09 80-126 BL00203 13.94 6.418e-09 55-101 BL00203 13.94 7.337e-09 15-61

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SEQ ID	Database entry ID	Description	Results*
			BL00203 13.94 7.337e-09 69-115 BL00203 13.94 7.520e-09 45-91 BL00203 13.94 7.888e-09 95-141 BL00203 13.94 8.255e-09 29-75 BL00203 13.94 8.439e-09 206-252 BL00203 13.94 8.531e-09 126-172 BL00203 13.94 8.806e-09 38-84 BL00203 13.94 8.898e-09 151-197 BL00203 13.94 9.265e-09 216-262 BL00203 13.94 9.449e-09 180-226
1317	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 9.757e-09 113-127
1317	BL00269	Mammalian defensins proteins.	BL00269C 16.52 6.425e-10 132-161 BL00269C 16.52 9.882e-09 21-50
1318	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 2.268e-10 107-121
1318	PR00874	FUNGI-IV METALLOTHIONEIN SIGNATURE	PR00874C 4.37 9.739e-10 95-110
1318	BL00427	Disintegrins proteins.	BL00427 13.93 2.274e-09 114-169
1318	PD00866	GLYCOPROTEIN PROTEIN SPIKE E2 PRECURSOR PEPLIMER.	PD00866L 3.73 6.564e-10 1-11 PD00866L 3.73 1.443e-09 33-43 PD00866L 3.73 2.770e-09 119-129 PD00866L 3.73 2.918e-09 12-22 PD00866L 3.73 2.918e-09 19-29
1318	BL01208	VWFC domain proteins.	BL01208B 15.83 2.946e-09 143-158
1318	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.	DM01724 8.14 7.465e-10 17-37 DM01724 8.14 4.434e-09 19-39 DM01724 8.14 6.684e-09 10-30
1318	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 8.763e-09 132-160
1318	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 1.724e-12 124-170 BL00203 13.94 2.034e-12 119-165 BL00203 13.94 4.207e-12 115-161 BL00203 13.94 4.931e-12 93-139 BL00203 13.94 3.275e-11 109-155 BL00203 13.94 3.967e-11 120-166 BL00203 13.94 3.298e-10 114-160 BL00203 13.94 4.064e-10 35-81 BL00203 13.94 4.447e-10 100-146 BL00203 13.94 5.117e-10 98-144 BL00203 13.94 7.989e-10 83-129 BL00203 13.94 9.426e-10 125-171 BL00203 13.94 2.929e-09 34-80 BL00203 13.94 2.929e-09 94-140 BL00203 13.94 3.663e-09 32-78 BL00203 13.94 4.490e-09 88-134 BL00203 13.94 4.582e-09 110-156 BL00203 13.94 4.673e-09 101-147 BL00203 13.94 4.857e-09 104-150 BL00203 13.94 5.592e-09 43-89 BL00203 13.94 6.694e-09 111-157 BL00203 13.94 8.898e-09 55-101 BL00203 13.94 9.082e-09 99-145
1318	BL00243	Integrins beta chain cysteine-rich	BL00243I 31.77 1.662e-10 68-111

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SEQ ID	Database entry ID	Description	Results*
		domain proteins.	BL00243I 31.77 3.912e-10 38-81 BL00243I 31.77 5.500e-10 58-101 BL00243I 31.77 8.941e-10 48-91 BL00243I 31.77 6.324e-09 25-68 BL00243I 31.77 7.465e-09 118-161 BL00243I 31.77 9.239e-09 61-104 BL00243I 31.77 9.620e-09 98-141
1319	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.800e-14 107-120 PD00066 13.92 2.800e-14 219-232 PD00066 13.92 4.000e-13 79-92 PD00066 13.92 4.000e-12 51-64 PD00066 13.92 9.143e-12 191-204 PD00066 13.92 2.038e-10 163-176
1319	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.250e-13 203-220 BL00028 16.07 8.650e-13 35-52 BL00028 16.07 9.550e-13 91-108 BL00028 16.07 3.739e-12 147-164 BL00028 16.07 4.522e-12 119-136 BL00028 16.07 4.462e-11 175-192 BL00028 16.07 8.500e-10 63-80
1319	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.706e-12 60-74 PR00048B 6.02 6.000e-12 104-114 PR00048B 6.02 1.000e-11 216-226 PR00048A 10.52 3.368e-11 88-102 PR00048B 6.02 7.231e-11 160-170 PR00048A 10.52 7.632e-11 32-46 PR00048B 6.02 1.000e-10 188-198 PR00048A 10.52 2.565e-10 172-186 PR00048A 10.52 2.957e-10 200-214 PR00048B 6.02 1.000e-09 48-58 PR00048A 10.52 4.240e-09 144-158 PR00048B 6.02 6.684e-09 76-86 PR00048B 6.02 7.632e-09 132-142 PR00048A 10.52 8.560e-09 116-130
1319	PD02462	PROTEIN BOLA TRANSCRIPTION REGULATION AC.	PD02462A 22.48 9.122e-09 168-203
1320	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 8.800e-15 4-26
1320	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.250e-09 4-48
1321	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 5.055e-11 71-117 BL00203 13.94 8.439e-09 146-192 BL00203 13.94 9.082e-09 53-99
1327	BL00799	Granulins proteins.	BL00799H 14.15 9.667e-09 18-59
1329	PF00711	Beta defensins.	PF00711 15.76 7.915e-11 60-93
1329	PR00858	CRUSTACEAN METALLOTHIONEIN SIGNATURE	PR00858B 5.93 1.479e-09 55-74
1329	BL00317	WAP-type 'four-disulfide core' domain proteins.	BL00317B 14.58 2.216e-09 63-85
1329	DM01724	kw ALLERGEN POLLEN CIM1 HOLLI.	DM01724 8.14 4.484e-12 19-39 DM01724 8.14 4.484e-12 23-43 DM01724 8.14 4.484e-12 27-47 DM01724 8.14 4.484e-12 31-51 DM01724 8.14 4.296e-10 35-55 DM01724 8.14 4.197e-09 11-31

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SEQ ID	Database entry ID	Description	Results*
			DM01724 8.14 5.382e-09 7-27 DM01724 8.14 6.803e-09 15-35
1329	PR00872	DIPTERA (DROSOPHILA) METALLOTHIONEIN SIGNATURE	PR00872A 5.17 7.409e-09 99-112
1329	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 7.429e-13 47-93 BL00203 13.94 1.989e-11 54-100 BL00203 13.94 3.967e-11 50-96 BL00203 13.94 8.372e-10 51-97 BL00203 13.94 8.947e-10 58-104 BL00203 13.94 1.184e-09 75-121 BL00203 13.94 3.204e-09 74-120 BL00203 13.94 3.663e-09 57-103 BL00203 13.94 4.673e-09 65-111 BL00203 13.94 5.592e-09 70-116 BL00203 13.94 6.786e-09 55-101 BL00203 13.94 7.429e-09 40-86
1329	BL00264	Neurohypophysial hormones proteins.	BL00264 8.98 7.632e-09 94-121
1329	PD00866	GLYCOPROTEIN PROTEIN SPIKE E2 PRECURSOR PEPLIMER.	PD00866L 3.73 7.709e-10 74-84 PD00866L 3.73 6.902e-09 4-14 PD00866L 3.73 9.262e-09 1-11
1329	DM00864	EGF-LIKE DOMAIN.	DM00864A 15.21 9.486e-09 9-30
1329	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 2.000e-11 57-100 BL00243I 31.77 5.897e-10 69-112 BL00243I 31.77 1.254e-09 60-103 BL00243I 31.77 7.465e-09 8-51 BL00243I 31.77 1.000e-08 16-59
1330	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 2.957e-10 175-226
1330	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 3.278e-09 70-90 DM01206B 10.69 4.418e-09 105-125
1330	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 5.291e-09 125-160
1330	PF00992	Troponin.	PF00992A 16.67 5.026e-09 183-218 PF00992A 16.67 8.934e-09 191-226
1330	BL00048	Protamine P1 proteins.	BL00048 6.39 7.107e-16 64-91 BL00048 6.39 9.196e-16 63-90 BL00048 6.39 1.132e-12 62-89 BL00048 6.39 2.059e-12 66-93 BL00048 6.39 3.250e-12 65-92 BL00048 6.39 7.618e-12 92-119 BL00048 6.39 2.625e-11 60-87 BL00048 6.39 6.500e-11 113-140 BL00048 6.39 6.750e-11 78-105 BL00048 6.39 6.875e-11 104-131 BL00048 6.39 7.125e-11 112-139 BL00048 6.39 8.625e-11 74-101 BL00048 6.39 2.539e-10 108-135 BL00048 6.39 4.434e-10 61-88 BL00048 6.39 5.855e-10 110-137 BL00048 6.39 6.921e-10 98-125 BL00048 6.39 7.158e-10 109-136 BL00048 6.39 7.750e-10 97-124 BL00048 6.39 8.105e-10 79-106 BL00048 6.39 8.579e-10 19-46

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SEQ ID	Database entry ID	Description	Results*
			BL00048 6.39 8.934e-10 94-121 BL00048 6.39 9.526e-10 103-130 BL00048 6.39 1.675e-09 101-128 BL00048 6.39 1.900e-09 73-100 BL00048 6.39 3.250e-09 81-108 BL00048 6.39 3.475e-09 111-138 BL00048 6.39 3.700e-09 82-109 BL00048 6.39 3.700e-09 96-123 BL00048 6.39 4.263e-09 99-126 BL00048 6.39 5.163e-09 107-134 BL00048 6.39 5.275e-09 67-94 BL00048 6.39 5.275e-09 80-107 BL00048 6.39 5.388e-09 49-76 BL00048 6.39 6.738e-09 116-143 BL00048 6.39 8.650e-09 52-79 BL00048 6.39 8.763e-09 18-45 BL00048 6.39 9.100e-09 21-48 BL00048 6.39 9.550e-09 76-103 BL00048 6.39 9.550e-09 100-127 BL00048 6.39 9.663e-09 102-129 BL00048 6.39 1.000e-08 77-104
1331	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 7.750e-09 74-92
1332	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 2.154e-28 83-127
1332	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE	PR00759B 11.26 3.323e-10 101-112 PR00759C 14.15 2.125e-09 111-127
1333	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.162e-34 8-47
1333	PD00066	PROTEIN ZINC-FINGER METAL-BINDL.	PD00066 13.92 2.800e-14 273-286 PD00066 13.92 2.800e-14 301-314 PD00066 13.92 2.800e-14 329-342 PD00066 13.92 2.800e-14 357-370 PD00066 13.92 5.500e-13 245-258 PD00066 13.92 1.783e-11 217-230 PD00066 13.92 8.043e-11 189-202
1333	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.850e-13 257-274 BL00028 16.07 2.957e-12 201-218 BL00028 16.07 4.522e-12 341-358 BL00028 16.07 5.304e-12 285-302 BL00028 16.07 1.346e-11 369-386 BL00028 16.07 2.038e-11 229-246 BL00028 16.07 4.900e-10 313-330
1333	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.286e-13 198-212 PR00048A 10.52 2.929e-13 254-268 PR00048A 10.52 2.929e-13 282-296 PR00048A 10.52 5.500e-13 366-380 PR00048B 6.02 6.400e-13 354-364 PR00048A 10.52 8.941e-12 226-240 PR00048B 6.02 1.000e-11 326-336 PR00048B 6.02 5.846e-11 242-252 PR00048A 10.52 6.211e-11 310-324 PR00048A 10.52 8.579e-11 338-352 PR00048B 6.02 9.308e-11

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SEQ ID	Database entry ID	Description	Results*
			270-280 PR00048B 6.02 7.750e-10 298-308 PR00048B 6.02 8.313e-10 214-224
1336	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 8.920e-09 333-347 PR00806B 4.28 9.640e-09 332-346
1337	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 8.920e-09 333-347 PR00806B 4.28 9.640e-09 332-346
1340	BL01221	PMP-22 / EMP / MP20 family proteins.	BL01221B 13.29 6.745e-09 54-68
1343	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 8.200e-12 208-231
1348	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 1.947e-10 316-326
1352	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973A 21.17 2.306e-13 66-103
1353	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 8.200e-10 190-204 PR00019A 11.19 7.667e-09 193-207
1356	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327B 19.84 2.091e-09 144-166
1356	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 7.652e-09 291-301
1357	PF01130	CD36 family.	PF01130D 26.65 1.955e-23 337-391 PF01130C 22.91 1.851e-18 255-305 PF01130B 21.40 1.537e-15 200-246
1359	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.480e-10 160-183 BL00290B 13.17 2.875e-09 226-244
1366	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007A 19.33 6.936e-13 274-301 PR00007C 15.60 9.250e-13 349-371 PR00007B 14.16 9.372e-13 301-321 PR00007D 9.64 5.500e-11 381-392
1366	BL01113	C1q domain proteins.	BL01113B 18.26 1.675e-24 280-316 BL01113A 17.99 4.194e-15 200-227 BL01113D 7.47 3.250e-13 383-393 BL01113A 17.99 3.919e-13 191-218 BL01113C 13.18 9.294e-12 349-369 BL01113A 17.99 5.500e-11 185-212 BL01113A 17.99 6.727e-11 182-209 BL01113A 17.99 8.773e-11 203-230 BL01113A 17.99 3.681e-10 188-215 BL01113A 17.99 6.936e-10 176-203 BL01113A 17.99 7.319e-10 194-221 BL01113A 17.99 4.635e-09 209-236 BL01113A 17.99 5.500e-09 179-206
1366	BL00420	Speract receptor repeat proteins domain proteins.	BL00420A 20.42 3.250e-12 185-214 BL00420A 20.42 2.623e-10 203-232 BL00420A 20.42 2.385e-09 191-220 BL00420A 20.42 6.400e-09 182-211 BL00420A 20.42 7.646e-09 188-217 BL00420A 20.42 8.200e-09 173-

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SEQ ID	Database entry ID	Description	Results*
			202
1366	PR00524	CHOLECYSTOKININ TYPE A RECEPTOR SIGNATURE	PR00524F 5.36 1.766e-09 200-214 PR00524F 5.36 8.564e-09 188-202
1367	PR00794	PANCREATIC RIBONUCLEASE FAMILY SIGNATURE	PR00794D 17.96 8.800e-17 94-117 PR00794A 14.47 6.897e-16 46-66 PR00794B 16.95 5.655e-14 66-86
1367	BL00127	Pancreatic ribonuclease family proteins.	BL00127B 26.57 9.357e-29 46-91 BL00127C 31.49 9.763e-22 82-126 BL00127A 12.84 8.200e-10 31-41
1368	BL00067	3-hydroxyacyl-CoA dehydrogenase proteins.	BL00067A 21.37 9.053e-10 53-84
1368	BL00677	D-amino acid oxidases proteins.	BL00677A 6.96 3.821e-09 55-68
1368	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 4.000e-09 57-89
1369	BL00067	3-hydroxyacyl-CoA dehydrogenase proteins.	BL00067A 21.37 9.053e-10 53-84
1369	BL00677	D-amino acid oxidases proteins.	BL00677A 6.96 3.821e-09 55-68
1369	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 4.000e-09 57-89
1371	PR00762	CHLORIDE CHANNEL SIGNATURE	PR00762C 9.29 5.200e-20 203-223 PR00762A 14.22 8.364e-19 108-126 PR00762D 11.29 9.379e-19 440-461 PR00762B 12.12 7.750e-16 139-159 PR00762E 12.07 2.286e-15 475-492 PR00762F 15.12 6.559e-15 493-513 PR00762G 14.13 1.692e-11 531-546
1371	PD00866	GLYCOPROTEIN PROTEIN SPIKE E2 PRECURSOR PEPLIMER.	PD00866L 3.73 3.951e-09 9-19
1371	PD00120	REPEAT PRECURSOR GLYCOPROTEIN EG.	PD00120A 12.94 4.750e-09 6-19
1372	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245A 18.03 4.349e-18 100-122
1372	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 2.800e-13 131-171
1372	PR00642	EDG1 ORPHAN RECEPTOR SIGNATURE	PR00642D 9.70 5.065e-12 89-104
1372	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237C 15.69 6.400e-09 145-168
1374	BL01022	PTR2 family proton/oligopeptide symporters proteins.	BL01022B 22.19 2.241e-15 74-120 BL01022A 11.58 2.212e-12 44-63 BL01022C 16.62 4.919e-10 160-184
1374	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 2.169e-09 20-30
1375	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE	PR00705A 10.55 4.000e-21 132-148 PR00705B 10.22 2.385e-10 276-287
1375	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.	BL00139D 9.24 1.818e-18 295-312 BL00139A 10.29 1.000e-14 132-142 BL00139C 9.23 2.800e-10 275-285
1375	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	PR00704C 11.88 6.162e-09 132-149
1376	PR00237	RHODOPSIN-LIKE GPCR	PR00237C 15.69 3.333e-12 111-

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SEQ ID	Database entry ID	Description	Results*
		SUPERFAMILY SIGNATURE	134 PR00237E 13.03 5.667e-11 193-217 PR00237F 13.57 1.474e-09 397-422 PR00237B 13.50 4.750e-09 66-88
1376	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 9.625e-19 97-137 BL00237C 13.19 8.846e-09 392-419 BL00237B 5.28 9.182e-09 201-213
1378	BL00649	G-protein coupled receptors family 2 proteins.	BL00649C 17.82 5.773e-10 325-351
1378	PR00249	SECRETIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00249C 17.08 4.130e-09 327-351
1380	PD01876	ANTIGEN MELANOMA-ASSOCIATED MULTIGENE FAMILY TUM.	PD01876A 12.01 2.964e-26 1-42 PD01876C 21.73 2.343e-25 99-152 PD01876B 14.18 2.500e-12 62-96
1382	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.	DM01724 8.14 3.789e-10 291-311
1382	PR00213	MYELIN P0 PROTEIN SIGNATURE	PR00213E 5.51 8.969e-09 263-288
1382	PD01849	CHORION CLASS PRECURSOR EGG SHELL REPEAT MULTIGEN.	PD01849C 11.22 9.625e-09 265-293
1388	BL00170	Cyclophilin-type peptidyl-prolyl cis-trans isomerase signatur.	BL00170B 20.97 1.000e-40 88-128 BL00170C 18.49 1.409e-37 135-180 BL00170A 17.08 6.850e-22 58-85
1388	PR00153	CYCLOPHILIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SIGNATURE	PR00153C 11.01 2.800e-18 136-152 PR00153B 11.57 8.500e-17 93-106 PR00153D 11.99 4.000e-16 151-164 PR00153A 12.98 4.789e-16 64-80 PR00153E 9.10 2.980e-10 164-180
1390	BL00237	G-protein coupled receptors proteins.	BL00237C 13.19 6.571e-16 147-174 BL00237A 27.68 2.976e-11 13-53 BL00237B 5.28 2.421e-10 102-114
1390	PR00529	GONADOTROPHIN RELEASING HORMONE RECEPTOR SIGNATURE	PR00529D 23.59 7.380e-13 2-18 PR00529H 10.07 1.000e-10 176-197 PR00529F 5.98 5.138e-10 75-90
1390	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237F 13.57 7.429e-15 152-177 PR00237E 13.03 3.250e-14 94-118 PR00237D 8.94 7.000e-09 58-80 PR00237G 19.63 8.116e-09 192-219
1390	PD02448	TRANSCRIPTION PROTEIN DNA-BINDIN.	PD02448A 9.37 9.195e-09 34-73
1392	BL00216	Sugar transport proteins.	BL00216B 27.64 3.732e-11 196-246
1393	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237C 15.69 9.333e-12 143-166
1393	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 3.200e-10 129-169
1393	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245A 18.03 2.429e-12 116-138 PR00245B 10.38 7.525e-11 216-231 PR00245E 12.40 2.019e-10 330-345 PR00245C 7.84 7.286e-10 277-293

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SEQ ID	Database entry ID	Description	Results*
1397	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 1.783e-09 585-604 PR00014A 8.22 3.045e-09 747-757 PR00014C 15.44 6.087e-09 683-702
1397	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 1.750e-12 1016-1047 BL00790I 20.01 6.125e-12 694-725 BL00790I 20.01 6.679e-09 596-627
1397	PR00096	GLUTAMINE AMIDOTRANSFERASE SUPERFAMILY SIGNATURE	PR00096B 9.72 9.827e-09 1063-1075
1401	PD00866	GLYCOPROTEIN PROTEIN SPIKE E2 PRECURSOR PEPLIMER.	PD00866L 3.73 8.820e-09 51-61
1402	PR00250	FUNGAL PHEROMONE MATING FACTOR STE2 GPCR SIGNATURE	PR00250G 9.58 9.746e-09 21-43
1404	PD01652	RECEPTOR CELL NK GLYCOPROTEIN IMMUNOGLOB.	PD01652A 15.35 6.625e-10 24-60 PD01652B 8.50 1.836e-09 14-66 PD01652B 8.50 4.021e-09 111-163
1409	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 8.250e-12 268-292
1409	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 3.842e-10 312-322
1409	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 5.500e-10 421-454 PD02870D 15.74 6.266e-09 182-217
1409	PR00021	SMALL PROLINE-RICH PROTEIN SIGNATURE	PR00021A 4.31 8.405e-09 496-509
1414	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 3.455e-18 46-71 BL00215B 10.44 8.714e-12 183-196 BL00215A 15.82 7.319e-11 143-168
1414	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 6.040e-09 74-96
1414	BL00439	Acyltransferases ChoActase / COT / CPT family proteins.	BL00439A 9.40 8.279e-09 318-335
1416	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270D 24.66 9.286e-12 12-48
1417	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 2.714e-10 42-51
1417	BL01282	BIR repeat proteins.	BL01282B 30.49 5.114e-09 23-62
1418	BL00604	Synaptophysin / synaptoporin proteins.	BL00604A 9.13 7.035e-29 41-96 BL00604E 8.32 4.759e-24 201-243 BL00604C 14.66 8.807e-17 134-166 BL00604B 9.95 5.154e-16 104-134 BL00604D 12.28 5.100e-14 166-201
1418	PR00220	SYNAPTOPHYSIN/SYNAPTOPORIN FAMILY SIGNATURE	PR00220A 10.93 1.353e-21 38-61 PR00220E 3.46 4.150e-18 216-235 PR00220D 8.32 4.575e-15 149-173 PR00220C 11.05 5.557e-14 117-142 PR00220B 15.48 2.703e-13 62-88
1421	BL01219	Ammonium transporters proteins.	BL01219D 11.63 2.957e-10 217-241 BL01219F 15.24 8.809e-09 289-314
1421	PR00342	RHESUS BLOOD GROUP PROTEIN	PR00342G 8.18 1.458e-19 220-239

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SEQ ID	Database entry ID	Description	Results*
		SIGNATURE	PR00342B 11.09 8.657e-13 61-79 PR00342D 8.46 2.857e-12 128-145 PR00342H 7.61 6.927e-11 250-273 PR00342C 10.10 4.770e-10 90-108 PR00342E 14.49 5.950e-10 151-175 PR00342F 7.02 1.556e-09 185-201 PR00342L 7.61 9.600e-09 352-378
1423	PR00794	PANCREATIC RIBONUCLEASE FAMILY SIGNATURE	PR00794C 17.32 8.071e-14 96-115 PR00794B 16.95 6.455e-13 71-91 PR00794A 14.47 9.538e-13 51-71 PR00794D 17.96 9.368e-10 117-140
1423	BL00127	Pancreatic ribonuclease family proteins.	BL00127B 26.57 2.895e-23 51-96 BL00127C 31.49 3.045e-11 105-149 BL00127A 12.84 2.161e-09 36-46
1426	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830A 8.41 1.143e-11 165-185
1426	BL00113	Adenylate kinase proteins.	BL00113A 12.74 4.462e-09 471-488
1426	BL00674	AAA-protein family proteins.	BL00674B 4.46 8.905e-09 467-489
1427	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 9.500e-11 74-88 PR00019A 11.19 5.696e-10 77-91 PR00019B 11.36 6.400e-10 25-39 PR00019B 11.36 5.320e-09 49-63
1427	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 8.043e-09 382-401
1437	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 6.850e-15 889-917 PD01719A 12.89 6.727e-13 643-671 PD01719A 12.89 1.913e-12 832-860 PD01719A 12.89 4.261e-12 701-729
1442	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 1.900e-11 106-120
1443	BL00353	HMG1/2 proteins.	BL00353B 11.47 1.643e-32 72-122
1443	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE	PR00886A 10.08 7.218e-18 37-60 PR00886B 9.88 1.750e-12 60-81 PR00886C 11.84 9.016e-12 104-123
1443	BL00649	G-protein coupled receptors family 2 proteins.	BL00649C 17.82 6.226e-11 286-312
1443	PR00249	SECRETIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00249C 17.08 1.783e-09 288-312 PR00249D 13.09 5.143e-09 327-353
1446	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.373e-09 781-814
1448	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 8.780e-09 402-435
1448	PF00761	Polyomavirus coat protein.	PF00761A 12.61 8.925e-09 1-26
1449	PR00180	CELLULAR RETINALDEHYDE-BINDING PROTEIN SIGNATURE	PR00180B 16.42 7.146e-09 236-261
1452	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 4.706e-24 132-155 PR00926E 11.70 7.000e-19 89-108 PR00926D 10.53 9.308e-17 41-60 PR00926F 17.75 9.859e-10 35-58

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SEQ ID	Database entry ID	Description	Results*
1452	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 8.235e-10 33-58 BL00215B 10.44 6.400e-09 79-92 BL00215B 10.44 8.200e-09 174-187
1452	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 7.652e-22 67-89 PR00927G 11.07 3.500e-15 178-194 PR00927F 11.79 6.211e-14 128-145 PR00927D 11.02 4.000e-13 26-40 PR00927B 14.66 2.597e-12 164-186 PR00927E 14.93 7.818e-11 162-184 PR00927A 7.98 9.667e-09 28-41
1456	BL00239	Receptor tyrosine kinase class II proteins.	BL00239B 25.15 1.000e-40 1037-1085 BL00239E 17.14 1.000e-40 1154-1204 BL00239F 28.15 1.750e-31 1208-1253 BL00239C 18.75 1.000e-24 1099-1122 BL00239D 16.81 2.884e-15 1124-1150
1456	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.900e-14 1182-1198 BL00107A 18.39 9.217e-14 1112-1143
1456	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 4.316e-23 1183-1206 PR00109B 12.27 4.857e-19 1112-1131 PR00109E 14.41 5.500e-16 1227-1250 PR00109C 12.85 4.000e-13 1164-1175 PR00109A 15.00 8.962e-11 1066-1080
1456	BL00790	Receptor tyrosine kinase class V proteins.	BL00790O 7.68 4.532e-18 1161-1194 BL00790K 9.30 5.091e-16 1010-1064 BL00790H 13.42 1.466e-15 830-856 BL00790M 8.74 9.203e-12 1103-1125 BL00790Q 15.61 5.200e-11 1219-1268 BL00790P 12.33 8.057e-10 1194-1219
1456	BL00240	Receptor tyrosine kinase class III proteins.	BL00240F 17.74 3.875e-26 1153-1201 BL00240C 22.58 4.414e-16 978-1027 BL00240E 11.56 5.061e-15 1098-1136 BL00240G 28.45 8.909e-10 1200-1253
1456	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 2.350e-09 893-908 PR00014B 14.77 7.000e-09 842-853
1456	BL50001	Src homology 2 (SH2) domain proteins profile.	BL50001B 17.40 9.640e-09 1109-1130
1457	PF01307	Plant virus coat protein.	PF01307A 21.19 3.025e-09 321-351
1462	BL00546	Matrixins cysteine switch.	BL00546C 16.41 1.643e-33 232-264 BL00546B 20.11 8.895e-29 18-62 BL00546A 19.62 7.667e-26 91-121 BL00546B 20.11 7.720e-19 180-224 BL00546D 10.34 1.000e-15 273-287 BL00546E 10.23 4.529e-15 309-330

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SEQ ID	Database entry ID	Description	Results*
1462	BL00024	Hemopexin domain proteins.	BL00024D 17.28 7.375e-34 232-264 BL00024C 22.98 5.091e-32 17-66 BL00024B 21.53 3.143e-23 130-164 BL00024C 22.98 8.732e-22 179-228 BL00024E 7.58 5.500e-15 273-287 BL00024F 11.30 1.900e-14 309-330 BL00024A 11.49 9.100e-13 111-122
1462	BL00142	Neutral zinc metalloproteinases, zinc-binding region proteins.	BL00142 8.38 1.000e-12 238-249
1462	PR00138	MATRIXIN SIGNATURE	PR00138D 16.56 6.500e-30 238-264 PR00138C 16.41 5.846e-16 18-47 PR00138A 15.14 7.136e-16 111-125 PR00138E 6.01 7.000e-15 273-287 PR00138B 15.82 3.824e-11 156-172
1462	PR00480	ASTACIN FAMILY SIGNATURE	PR00480B 15.41 6.045e-10 233-252
1475	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354Z 9.06 9.566e-17 216-265 DM01354Z 9.06 2.534e-15 161-210
1478	PR00185	EUKARYOTIC PORIN SIGNATURE	PR00185D 16.54 1.136e-11 111-129
1482	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449E 13.50 4.971e-11 464-487
1484	PR00879	FISH ACETYLCHOLINESTERASE SIGNATURE	PR00879A 6.28 1.000e-08 39-45
1487	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354Q 9.23 1.000e-40 283-338 DM01354T 9.48 4.882e-39 389-432 DM01354R 8.50 8.380e-28 338-368 DM01354P 9.18 2.957e-26 249-283 DM01354S 11.61 1.000e-18 368-389
1489	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327C 15.47 3.538e-09 60-75
1491	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354B 14.71 6.426e-14 271-299
1493	PR00502	MUTT DOMAIN SIGNATURE	PR00502B 15.92 4.643e-09 348-364
1494	PF00997	Kappa casein.	PF00997D 9.95 8.306e-09 117-152
1495	DM01162	BARLEY YELLOW DWARF VIRUS RNA-DIRECTED RNA POLYMERASE.	DM01162B 11.50 9.743e-09 104-113
1497	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 9.757e-10 79-113
1498	PR00069	ALDO-KETO REDUCTASE SIGNATURE	PR00069D 19.36 1.659e-19 260-290
1498	BL00798	Aldo/keto reductase family proteins.	BL00798F 23.30 5.125e-25 314-363 BL00798E 20.32 7.462e-24 256-294 BL00798A 14.97 3.000e-10 207-222
1499	BL00826	MARCKS family proteins.	BL00826B 12.51 2.116e-09 545-597
1499	BL00970	Nuclear transition protein 2 proteins.	BL00970C 14.80 5.538e-09 567-605
1499	DM00303	6 LEA 11-MER REPEAT REPEAT.	DM00303A 13.20 8.327e-09 574-

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SEQ ID	Database entry ID	Description	Results*
			624
1499	PD01457	RIBOSOMAL PROTEIN 40S ZINC-FINGER METAL.	PD01457A 16.51 7.708e-11 561-606 PD01457A 16.51 1.409e-10 565-610 PD01457A 16.51 5.745e-10 559-604 PD01457A 16.51 2.397e-09 558-603 PD01457A 16.51 3.483e-09 567-612 PD01457A 16.51 4.103e-09 560-605 PD01457A 16.51 8.060e-09 563-608 PD01457A 16.51 8.293e-09 557-602 PD01457A 16.51 8.914e-09 562-607
1499	BL00348	p53 tumor antigen proteins.	BL00348F 23.19 5.571e-09 543-586 BL00348F 23.19 6.429e-09 583-626 BL00348F 23.19 9.286e-09 560-603
1501	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354X 13.86 6.230e-15 3-42
1502	BL01210	Caveolins proteins.	BL01210A 17.61 9.438e-14 132-171
1503	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.571e-10 65-80
1503	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.161e-10 53-86 DM00215 19.43 8.393e-10 52-85 DM00215 19.43 4.661e-09 47-80 DM00215 19.43 5.729e-09 46-79
1506	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354Z 9.06 8.548e-13 66-115
1508	PD01941	TRANSMEMBRANE COTRANSPORTER SYMP.	PD01941E 15.92 8.714e-23 198-245 PD01941F 28.52 5.154e-11 496-551
1510	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354N 13.17 1.000e-40 148-193 DM01354V 12.97 1.000e-40 274-321 DM01354V 12.97 6.932e-40 218-265 DM01354O 8.73 1.882e-19 199-245 DM01354W 12.64 2.427e-13 265-285 DM01354W 12.64 1.300e-11 321-341
1511	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.913e-19 230-269
1511	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.600e-13 343-360 BL00028 16.07 6.087e-12 371-388
1511	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.250e-16 340-354 PR00048A 10.52 3.348e-10 368-382 PR00048B 6.02 4.938e-10 384-394
1511	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.077e-10 331-344 PD00066 13.92 6.700e-09 359-372
1517	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.875e-15 449-466 BL00028 16.07 6.824e-14 309-326 BL00028 16.07 7.353e-14 505-522 BL00028 16.07 2.800e-13 1038-1055 BL00028 16.07 8.650e-13 337-354 BL00028 16.07 1.783e-12 926-943 BL00028 16.07 4.913e-12

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SEQ ID	Database entry ID	Description	Results*
			982-999 BL00028 16.07 5.304e-12 898-915 BL00028 16.07 5.304e-12 1094-1111 BL00028 16.07 8.435e-12 421-438 BL00028 16.07 3.077e-11 393-410 BL00028 16.07 3.423e-11 954-971 BL00028 16.07 3.769e-11 365-382 BL00028 16.07 4.462e-11 870-887 BL00028 16.07 5.154e-11 281-298 BL00028 16.07 4.000e-10 477-494 BL00028 16.07 7.000e-10 1010-1027 BL00028 16.07 7.000e-10 1066-1083
1517	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.400e-30 76-115 PD01066 19.43 7.525e-15 675-714 PD01066 19.43 1.943e-09 716-755
1517	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.500e-16 446-460 PR00048A 10.52 9.182e-15 306-320 PR00048A 10.52 9.182e-15 1035-1049 PR00048A 10.52 5.500e-14 502-516 PR00048A 10.52 7.750e-14 923-937 PR00048A 10.52 1.643e-13 895-909 PR00048A 10.52 4.214e-13 1091-1105 PR00048A 10.52 4.857e-13 334-348 PR00048A 10.52 4.706e-12 362-376 PR00048B 6.02 5.000e-12 434-444 PR00048A 10.52 6.294e-12 474-488 PR00048A 10.52 9.471e-12 951-965 PR00048A 10.52 3.842e-11 979-993 PR00048A 10.52 4.789e-11 418-432 PR00048B 6.02 9.308e-11 1023-1033 PR00048B 6.02 1.563e-10 294-304 PR00048B 6.02 1.563e-10 883-893 PR00048B 6.02 2.125e-10 911-921 PR00048B 6.02 2.688e-10 350-360 PR00048B 6.02 8.313e-10 939-949 PR00048B 6.02 9.438e-10 490-500 PR00048B 6.02 1.000e-09 995-1005 PR00048B 6.02 3.368e-09 462-472 PR00048A 10.52 3.880e-09 390-404 PR00048B 6.02 4.316e-09 1079-1089 PR00048A 10.52 4.600e-09 867-881
1517	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.800e-14 325-338 PD00066 13.92 4.600e-14 437-450 PD00066 13.92 5.200e-14 998-1011 PD00066 13.92 6.400e-14 493-506 PD00066 13.92 8.800e-14 942-955 PD00066 13.92 5.500e-13 1026-1039 PD00066 13.92 6.000e-13 970-983 PD00066 13.92 6.500e-13 297-310 PD00066 13.92 6.500e-13 886-899 PD00066 13.92 7.000e-13 465-478 PD00066 13.92

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SEQ ID	Database entry ID	Description	Results*
			7.000e-13 914-927 PD00066 13.92 9.000e-13 353-366 PD00066 13.92 9.500e-13 1082-1095 PD00066 13.92 4.808e-10 409-422 PD00066 13.92 4.000e-09 381-394 PD00066 13.92 5.800e-09 1054-1067
1517	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479A 19.86 7.319e-09 1025-1048
1518	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.158e-13 42-65 BL00290B 13.17 4.500e-12 98-116
1519	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354K 9.35 7.706e-28 71-103 DM01354L 11.73 8.250e-14 103-130
1521	BL00250	TGF-beta family proteins.	BL00250A 21.24 2.500e-31 640-676 BL00250B 27.37 2.000e-27 705-741
1521	BL01273	CoA transferases proteins.	BL01273C 12.54 1.000e-40 130-170 BL01273D 19.11 9.471e-28 206-250 BL01273B 14.85 9.830e-20 81-115 BL01273A 12.56 2.286e-16 62-75
1521	PR00669	INHIBIN ALPHA CHAIN SIGNATURE	PR00669E 16.28 7.078e-12 640-658
1523	BL00427	Disintegrins proteins.	BL00427 13.93 4.100e-15 455-510
1523	PR00289	DISINTEGRIN SIGNATURE	PR00289A 13.62 3.700e-18 469-489 PR00289B 11.79 3.143e-12 498-511
1523	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 9.870e-09 675-694
1524	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 8.683e-12 186-197
1524	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 3.100e-09 183-202
1525	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237G 19.63 7.000e-17 35-62
1525	BL00237	G-protein coupled receptors proteins.	BL00237D 11.23 3.500e-14 45-62
1525	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR00424F 8.50 2.688e-12 35-46
1525	PR00554	ADENOSINE A2B RECEPTOR SIGNATURE	PR00554F 8.86 1.750e-16 24-37 PR00554G 14.18 7.288e-12 69-89
1528	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 9.217e-09 338-351
1530	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354N 13.17 1.000e-40 36-81 DM01354O 8.73 1.000e-40 87-133 DM01354Q 9.23 1.000e-40 167-222 DM01354T 9.48 1.000e-40 273-316 DM01354V 12.97 1.000e-40 382-429 DM01354Y 10.69 1.000e-40 498-538 DM01354X 13.86 5.219e-39 449-488 DM01354P 9.18 2.723e-37 133-167 DM01354R 8.50 7.395e-32 222-252 DM01354W 12.64 3.000e-25 429-449 DM01354S 11.61 9.550e-23 252-273 DM01354U 12.24 2.350e-20 362-382

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SEQ ID	Database entry ID	Description	Results*
1530	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895E 15.72 3.889e-11 149-174
1532	PR00036	LACI BACTERIAL REGULATORY PROTEIN HTH SIGNATURE	PR00036B 10.57 1.000e-08 282-293
1533	BL01160	Kinesin light chain repeat proteins.	BL01160D 10.17 7.077e-09 218-247
1533	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 1.000e-08 485-506
1535	PR00671	INHIBIN BETA B CHAIN SIGNATURE	PR00671C 4.18 9.690e-09 44-64
1538	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 9.217e-14 89-120 BL00107B 13.31 6.786e-11 159-175
1538	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 6.766e-09 89-108
1539	PR00502	MUTT DOMAIN SIGNATURE	PR00502B 15.92 7.000e-09 131-147
1540	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 1.786e-10 813-828
1541	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418A 20.83 1.000e-40 631-679 DM01418C 20.48 1.000e-40 800-842 DM01418B 22.51 4.103e-38 729-771
1541	BL00420	Speract receptor repeat proteins domain proteins.	BL00420A 20.42 2.180e-10 549-578
1541	BL01113	C1q domain proteins.	BL01113A 17.99 1.957e-10 555-582 BL01113A 17.99 2.149e-10 549-576 BL01113A 17.99 7.319e-10 552-579
1542	BL00279	Membrane attack complex components / perforin proteins.	BL00279E 37.11 9.053e-12 901-949
1542	PR00907	THROMBOMODULIN SIGNATURE	PR00907B 11.29 8.274e-11 1016-1033
1542	PR00764	COMPLEMENT C9 SIGNATURE	PR00764F 16.89 3.836e-10 918-939
1542	DM00864	EGF-LIKE DOMAIN.	DM00864B 11.34 6.910e-10 1025-1044
1542	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 4.150e-14 1020-1036 BL01187B 12.04 2.575e-09 927-943
1542	BL01177	Anaphylatoxin domain proteins.	BL01177E 20.64 7.632e-09 1018-1045
1542	BL00799	Granulins proteins.	BL00799B 11.02 9.679e-09 1011-1047
1542	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010A 11.79 5.154e-11 912-924 PR00010C 11.16 7.545e-10 1025-1036 PR00010C 11.16 9.786e-09 932-943
1543	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 7.038e-09 79-113
1544	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 6.318e-19 478-496 BL00972D 22.55 7.968e-16 762-787 BL00972B 9.45 1.600e-12 559-569
1544	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.008e-13 235-250 PR00049D 0.00 7.375e-12 239-254

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SEQ ID	Database entry ID	Description	Results*
			PR00049D 0.00 5.916e-11 242-257 PR00049D 0.00 6.748e-11 236-251 PR00049D 0.00 9.395e-11 240-255 PR00049D 0.00 1.286e-10 233-248 PR00049D 0.00 8.929e-10 241-256 PR00049D 0.00 2.678e-09 243-258 PR00049D 0.00 4.051e-09 237-252 PR00049D 0.00 4.051e-09 238-253 PR00049D 0.00 4.051e-09 244-259
1544	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 7.500e-09 238-259
1544	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 5.339e-10 222-255 DM00215 19.43 7.268e-10 226-259 DM00215 19.43 2.525e-09 220-253 DM00215 19.43 9.695e-09 221-254
1544	BL00048	Protamine P1 proteins.	BL00048 6.39 9.888e-09 259-286
1546	PR00416	EUKARYOTIC DNA TOPOISOMERASE I SIGNATURE	PR00416B 15.58 5.000e-09 389-409
1546	BL00048	Protamine P1 proteins.	BL00048 6.39 8.200e-09 510-537
1546	PR00138	MATRIXIN SIGNATURE	PR00138E 6.01 8.429e-09 146-160
1546	BL00024	Hemopexin domain proteins.	BL00024E 7.58 8.694e-09 146-160
1546	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 4.857e-12 317-331 PR00019A 11.19 8.333e-09 133-147 PR00019B 11.36 8.920e-09 269-283
1547	DM01595	kw ALLANTOICASE SPAC1F7.09C.	DM01595B 10.54 2.625e-15 143-171 DM01595I 8.91 2.714e-15 457-475 DM01595D 10.94 3.274e-11 456-481
1549	PR00192	F-ACTIN CAPPING PROTEIN BETA SUBUNIT SIGNATURE	PR00192A 8.23 1.474e-27 47-68
1549	BL00231	F-actin capping protein beta subunit proteins.	BL00231A 8.59 1.829e-24 47-93
1551	BL00708	Prolyl endopeptidase family serine proteins.	BL00708B 24.91 7.197e-12 439-470
1551	PF00930	Dipeptidyl peptidase IV (DPP IV) N-terminal region.	PF00930I 15.96 6.373e-17 481-509 PF00930H 20.16 2.482e-13 402-445 PF00930J 8.78 1.000e-11 533-554 PF00930G 21.30 9.613e-09 362-400
1552	BL00878	Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment si.	BL00878F 19.67 7.231e-20 171-194 BL00878C 17.74 3.676e-11 38-58
1552	PR00163	RUBREDOXIN SIGNATURE	PR00163B 14.45 8.200e-09 143-160
1555	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354V 12.97 1.000e-40 705-752 DM01354U 12.24 6.700e-22 685-705 DM01354T 9.48 8.355e-15 596-639 DM01354W 12.64 9.122e-13 752-772
1557	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354N 13.17 1.000e-40 158-203 DM01354O 8.73 1.000e-40 209-255 DM01354Q 9.23 1.000e-40 289-344 DM01354T 9.48 1.000e-40 398-441 DM01354V 12.97 1.000e-40 507-554 DM01354P 9.18 5.213e-37 255-289

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SEQ ID	Database entry ID	Description	Results*
			DM01354R 8.50 6.760e-28 344-374 DM01354L 11.73 1.200e-26 101-128 DM01354S 11.61 7.300e-26 377-398 DM01354M 12.50 6.094e-24 128-158 DM01354U 12.24 6.700e-22 487-507 DM01354K 9.35 1.228e-17 69-101 DM01354W 12.64 1.000e-13 554-574
1557	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895E 15.72 7.828e-10 271-296
1558	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE	PR00834F 10.91 2.946e-09 194-207
1558	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 2.962e-09 1104-1127
1558	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 4.814e-09 1318-1333 PR00049D 0.00 5.729e-09 259-274
1558	PR00554	ADENOSINE A2B RECEPTOR SIGNATURE	PR00554B 12.52 8.855e-09 917-926
1560	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 3.700e-10 977-1012
1565	BL01226	Hydroxymethylglutaryl-coenzyme A synthase proteins.	BL01226A 13.79 1.000e-40 50-89 BL01226C 13.51 1.000e-40 127-167 BL01226H 17.74 1.000e-40 478-526 BL01226G 15.76 3.483e-32 384-413 BL01226B 13.35 1.818e-31 95-127 BL01226F 9.78 8.714e-23 345-363 BL01226E 13.74 7.716e-22 304-345 BL01226D 11.60 5.680e-18 226-262 BL01226D 11.60 6.940e-10 174-210
1568	BL00189	2-oxo acid dehydrogenases acyltransferase component lipoyl bi.	BL00189A 19.58 4.414e-13 103-138
1574	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 4.661e-09 254-269
1574	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 6.241e-09 184-199
1577	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE	PR00756B 14.06 2.364e-13 232-248 PR00756C 11.60 7.300e-12 310-321
1579	BL00048	Protamine P1 proteins.	BL00048 6.39 3.605e-10 636-663 BL00048 6.39 5.500e-10 630-657 BL00048 6.39 1.225e-09 628-655 BL00048 6.39 4.263e-09 648-675 BL00048 6.39 5.388e-09 627-654 BL00048 6.39 8.988e-09 626-653
1580	BL00284	Serpins proteins.	BL00284C 28.56 5.821e-27 192-234 BL00284A 15.64 1.000e-18 63-87 BL00284D 16.34 1.500e-14 407-434 BL00284B 17.99 1.273e-12 162-183
1581	BL01052	Calponin family repeat proteins.	BL01052B 15.31 3.308e-11 110-136
1581	PR00888	SMOOTH MUSCLE	PR00888C 12.27 2.141e-09 110-

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SEQ ID	Database entry ID	Description	Results*
		PROTEIN/CALPONIN FAMILY SIGNATURE	126
1582	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 6.500e-11 140-154 PR00019B 11.36 7.750e-10 92-106 PR00019A 11.19 5.000e-09 95-109
1582	PR00423	CELL DIVISION PROTEIN FTSZ SIGNATURE	PR00423E 7.36 9.550e-09 505-527
1587	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.500e-10 277-294
1587	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 8.286e-10 186-195
1588	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354R 8.50 7.750e-29 192-222 DM01354S 11.61 7.300e-26 222-243
1589	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354U 12.24 5.891e-19 62-82 DM01354V 12.97 1.175e-09 82-129
1590	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354Z 9.06 5.065e-13 167-216
1591	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354R 8.50 1.840e-18 141-171
1591	BL00300	SRP54-type proteins GTP-binding domain proteins.	BL00300C 25.57 7.100e-09 648-702
1593	BL00573	Pyridine nucleotide-disulphide oxidoreductases class-II activ.	BL00573A 9.65 7.273e-10 750-768
1593	PR00411	PYRIDINE NUCLEOTIDE DISULPHIDE REDUCTASE CLASS-I SIGNATURE	PR00411A 15.95 4.569e-09 747-770
1593	PR00350	VITAMIN D RECEPTOR SIGNATURE	PR00350E 11.55 5.546e-09 13-33
1593	PR00368	FAD-DEPENDENT PYRIDINE NUCLEOTIDE REDUCTASE SIGNATURE	PR00368A 17.76 7.589e-09 747-770
1593	BL01113	C1q domain proteins.	BL01113A 17.99 9.827e-09 484-511
1593	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.892e-10 373-383 PR00308C 3.83 1.701e-09 375-385 PR00308A 5.90 4.282e-09 752-767 PR00308A 5.90 6.824e-09 372-387 PR00308C 3.83 1.000e-08 324-334
1594	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354X 13.86 6.595e-36 13-52 DM01354Y 10.69 3.455e-09 62-102
1595	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE	PR00756D 10.58 7.000e-19 187-203 PR00756E 11.91 3.700e-15 206-219 PR00756C 11.60 4.000e-12 151-162
1595	BL00142	Neutral zinc metalloproteases, zinc-binding region proteins.	BL00142 8.38 2.286e-09 187-198
1596	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354I 15.55 1.000e-40 119-160 DM01354V 12.97 1.209e-14 401-448 DM01354H 18.00 5.280e-10 79-119
1600	BL00484	Thyroglobulin type-1 repeat proteins.	BL00484C 17.01 3.854e-11 96-111

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SEQ ID	Database entry ID	Description	Results*
1601	PR00342	RHESUS BLOOD GROUP PROTEIN SIGNATURE	PR00342A 9.71 1.000e-23 12-31
1608	PD01941	TRANSMEMBRANE COTRANSPORTER SYMP.	PD01941E 15.92 1.000e-40 135-182 PD01941F 28.52 9.229e-17 254-309
1609	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354W 12.64 9.375e-16 123-143
1614	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 5.808e-26 49-104 BL00420C 11.90 2.500e-10 134-145
1614	PR00258	SPERACT RECEPTOR SIGNATURE	PR00258B 9.63 7.947e-11 64-76 PR00258C 9.05 3.204e-10 79-90 PR00258E 13.33 3.333e-10 133-146 PR00258D 14.41 3.286e-09 110-125
1616	BL00326	Tropomyosins proteins.	BL00326D 8.76 1.505e-09 377-418
1616	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE	PR00261D 12.47 3.338e-10 43-65 PR00261E 11.08 4.575e-10 84-106 PR00261C 11.37 5.050e-10 43-65 PR00261F 11.57 5.920e-10 43-65 PR00261A 11.02 6.769e-10 43-65 PR00261A 11.02 9.192e-10 84-106 PR00261D 12.47 2.667e-09 84-106 PR00261F 11.57 4.304e-09 84-106 PR00261C 11.37 5.500e-09 84-106 PR00261B 14.12 5.714e-09 84-106 PR00261B 14.12 6.464e-09 43-65
1616	BL01209	LDL-receptor class A (LDLRA) domain proteins.	BL01209 9.31 6.464e-09 93-106
1616	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.613e-13 306-357 BL00412D 16.54 8.821e-12 301-352 BL00412D 16.54 1.098e-10 307-358 BL00412D 16.54 9.609e-10 304-355 BL00412D 16.54 1.184e-09 308-359 BL00412D 16.54 1.918e-09 309-360 BL00412D 16.54 2.745e-09 302-353 BL00412D 16.54 5.684e-09 299-350 BL00412D 16.54 8.347e-09 303-354
1616	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 8.640e-09 319-354
1616	BL00422	Granins proteins.	BL00422C 16.18 8.085e-10 326-354 BL00422C 16.18 8.468e-10 330-358 BL00422C 16.18 8.851e-10 323-351 BL00422C 16.18 4.529e-09 325-353 BL00422C 16.18 9.471e-09 318-346
1618	PR00681	RIBOSOMAL PROTEIN S1 SIGNATURE	PR00681I 8.81 9.897e-09 412-431
1619	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 3.813e-15 55-72
1619	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722A 12.27 8.448e-14 56-72
1619	BL00021	Kringle domain proteins.	BL00021B 13.33 1.763e-13 55-73

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SEQ ID	Database entry ID	Description	Results*
1619	PR00839	V8 SERINE PROTEASE FAMILY SIGNATURE	PR00839B 11.20 4.945e-09 55-73
1620	BL00125	Serine/threonine specific protein phosphatases proteins.	BL00125C 19.97 1.000e-40 86-133 BL00125D 33.11 9.679e-38 154-209
1620	PR00114	SERINE/THREONINE PHOSPHATASE FAMILY SIGNATURE	PR00114E 17.75 2.500e-27 106-134 PR00114D 12.34 9.591e-26 77-104 PR00114F 17.51 3.400e-17 170-191 PR00114G 17.20 3.676e-17 198-215
1625	BL01103	Aspartate-semialdehyde dehydrogenase proteins.	BL01103F 16.78 3.625e-24 256-282 BL01103C 15.07 6.727e-20 91-113 BL01103B 20.29 5.846e-16 51-73 BL01103E 11.30 4.115e-14 238-251 BL01103D 7.29 1.000e-09 155-166
1626	PD02410	SYNTHETASE BETA CHAIN LIGASE PHENYLALANYL-TRNA.	PD02410E 10.29 2.241e-13 83-97
1628	BL00044	Bacterial regulatory proteins, lysR family proteins.	BL00044 19.03 7.188e-11 21-55
1631	BL00370	PEP-utilizing enzymes phosphorylation site proteins proteins.	BL00370C 11.73 9.182e-17 96-110
1632	PR00101	ASPARTATE CARBAMOYLTRANSFERASE SIGNATURE	PR00101C 12.35 9.328e-10 410-428
1632	BL00097	Aspartate and ornithine carbamoyltransferases proteins.	BL00097C 16.87 1.621e-09 411-425
1634	BL00530	Ribonuclease T2 family histidine proteins 1.	BL00530C 11.43 1.000e-17 101-113
1643	BL00050	Ribosomal protein L23 proteins.	BL00050A 23.71 3.659e-18 217-250
1645	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 5.571e-14 479-507 PD01719A 12.89 2.000e-09 666-694 PD01719A 12.89 4.889e-09 606-634 PD01719A 12.89 8.111e-09 419-447
1647	BL00564	Argininosuccinate synthase proteins.	BL00564D 22.43 2.723e-22 157-194 BL00564A 19.93 6.582e-11 37-74
1651	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE	PR00453A 12.79 9.719e-13 88-106 PR00453B 14.65 1.818e-12 125-140 PR00453C 12.26 3.769e-10 246-255
1652	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 9.471e-27 84-118 DM00031A 16.80 7.055e-25 206-254 DM00031A 16.80 5.368e-18 20-68 DM00031B 15.41 8.519e-09 267-301
1653	PR00173	GLUTAMATE-ASPARTATE SYMPORTER SIGNATURE	PR00173F 10.44 8.967e-09 8-28
1654	BL01032	Protein phosphatase 2C proteins.	BL01032C 6.14 1.000e-10 118-128
1657	BL00523	Sulfatases proteins.	BL00523A 13.36 2.200e-13 47-64
1658	BL00194	Thioredoxin family proteins.	BL00194 12.16 4.857e-16 482-495 BL00194 12.16 3.813e-15 347-360
1658	PR00421	THIOREDOXIN FAMILY SIGNATURE	PR00421B 11.40 3.348e-12 489-499 PR00421B 11.40 9.379e-11

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SEQ ID	Database entry ID	Description	Results*
			354-364 PR00421A 10.15 4.000e-10 346-355 PR00421A 10.15 4.857e-10 481-490 PR00421C 13.60 5.714e-10 533-545
1662	PF00850	Histone deacetylase family.	PF00850E 8.88 1.766e-21 1269-1295 PF00850F 15.70 1.889e-10 1307-1340 PF00850G 22.75 3.724e-10 1346-1388
1666	BL00317	WAP-type 'four-disulfide core' domain proteins.	BL00317B 14.58 7.231e-22 92-114
1666	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003C 7.69 6.885e-11 98-108 PR00003D 8.10 4.971e-09 108-117
1666	BL00313	Seminal vesicle protein I repeat proteins proteins.	BL00313B 8.87 1.000e-40 31-68 BL00313C 11.19 1.000e-18 103-118 BL00313B 8.87 5.337e-17 25-62 BL00313B 8.87 7.593e-16 19-56 BL00313B 8.87 1.910e-15 43-80 BL00313B 8.87 9.413e-14 37-74 BL00313B 8.87 4.522e-09 49-86 BL00313A 10.60 5.500e-09 1-9 BL00313C 11.19 9.060e-09 30-45
1667	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.395e-31 108-147
1667	BL01277	Ribonuclease PH proteins.	BL01277A 17.39 8.818e-09 64-102
1672	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.	DM00372B 20.31 8.920e-15 363-408 DM00372B 20.31 3.329e-12 68-113
1673	PF00992	Troponin.	PF00992A 16.67 8.859e-10 176-211
1673	BL00093	N-4 cytosine-specific DNA methylases proteins.	BL00093A 9.77 4.329e-09 718-733
1673	PR00948	ELICITIN SIGNATURE	PR00948B 15.44 5.361e-08 707-732
1673	PR00558	ALPHA-2A ADRENERGIC RECEPTOR SIGNATURE	PR00558C 6.54 6.719e-08 429-449
1676	BL00962	Ribosomal protein S2 proteins.	BL00962B 36.15 6.529e-14 53-107
1678	PD00015	GLYCOPROTEIN PRECURSOR CELL SI.	PD00015A 8.90 6.400e-09 35-43
1678	PR00795	RYANODINE RECEPTOR SIGNATURE	PR00795C 6.30 8.252e-09 107-132
1683	BL00262	Insulin family proteins.	BL00262A 12.48 3.829e-09 30-48
1684	BL00061	Short-chain dehydrogenases/reductases family proteins.	BL00061B 25.79 8.105e-19 133-171
1684	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE	PR00080C 17.16 2.125e-10 153-173
1684	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081A 10.53 7.805e-11 5-23 PR00081C 15.13 1.771e-09 127-144
1685	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 6.885e-09 197-213
1686	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 7.158e-18 678-709
1686	PR00653	ACTIVIN TYPE II RECEPTOR SIGNATURE	PR00653E 15.68 5.114e-16 871-891 PR00653D 13.25 7.195e-12 697-719
1686	BL00790	Receptor tyrosine kinase class V	BL00790N 13.25 7.505e-09 691-

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SEQ ID	Database entry ID	Description	Results*
		proteins.	718
1686	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 8.031e-09 678-697
1687	BL00649	G-protein coupled receptors family 2 proteins.	BL00649A 24.05 2.333e-22 85-113
1687	PR00491	VASOACTIVE INTESTINAL PEPTIDE RECEPTOR SIGNATURE	PR00491A 11.52 9.509e-10 109-121
1688	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 2.500e-18 154-173
1688	PR00401	SH2 DOMAIN SIGNATURE	PR00401A 14.00 5.765e-15 214-229
1688	BL50001	Src homology 2 (SH2) domain proteins profile.	BL50001A 10.81 6.250e-11 154-167
1688	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 5.765e-14 164-180 PR00452A 10.48 8.500e-12 150-161 PR00452C 10.78 1.000e-10 181-191
1688	PR00499	NEUTROPHIL CYTOSOL FACTOR 2 SIGNATURE	PR00499D 10.18 7.279e-09 152-173
1693	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551A 15.63 7.265e-09 559-589
1693	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.957e-10 614-628 PR00019B 11.36 4.600e-10 527-541 PR00019B 11.36 1.720e-09 611-625 PR00019A 11.19 3.000e-09 660-674 PR00019A 11.19 7.667e-09 530-544
1698	PR00528	GLUCOCORTICOID RECEPTOR SIGNATURE	PR00528C 14.75 9.438e-09 210-231
1705	BL00733	Ribosomal protein S26e proteins.	BL00733B 12.04 4.661e-25 165-198
1706	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 6.500e-11 412-425
1706	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.000e-11 773-787 PR00019A 11.19 7.000e-09 776-790
1706	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 6.242e-13 386-441 PF00791C 20.98 7.088e-09 436-475 PF00791B 28.49 7.936e-09 455-510
1706	PF00023	Ank repeat proteins.	PF00023A 16.03 1.000e-11 419-435 PF00023B 14.20 9.591e-09 415-425
1708	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.000e-13 251-264 PD00066 13.92 3.571e-12 223-236
1708	PR00498	NEUTROPHIL CYTOSOL FACTOR 1 SIGNATURE	PR00498A 12.01 5.765e-09 353-362
1708	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048B 6.02 1.563e-10 220-230 PR00048A 10.52 2.565e-10 232-246 PR00048A 10.52 5.320e-09 50-64 PR00048A 10.52 8.200e-09 204-218
1708	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.154e-11 235-252 BL00028 16.07 3.400e-10 207-224 BL00028 16.07 9.743e-09 53-70
1711	PF00550	Phosphopantetheine attachment site	PF00550C 13.05 7.188e-10 235-

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SEQ ID	Database entry ID	Description	Results*
		proteins.	252
1712	BL00484	Thyroglobulin type-1 repeat proteins	BL00484B 9.04 4.400e-12 289-303
1712	BL00222	Insulin-like growth factor binding proteins.	BL00222B 11.09 7.300e-17 65-81 BL00222A 11.34 9.438e-11 45-56
1715	PF00075	RNase H.	PF00075C 11.58 6.786e-13 60-72
1717	BL00477	Alpha-2-macroglobulin family thiolester region proteins.	BL00477G 19.43 3.739e-34 984-1016 BL00477A 13.50 6.000e-32 174-203 BL00477J 19.04 9.625e-31 1301-1332 BL00477F 17.34 1.931e-30 840-870 BL00477L 23.51 1.964e-30 1498-1531 BL00477K 17.42 6.400e-24 1443-1467 BL00477E 17.53 7.000e-22 810-831 BL00477I 18.76 6.750e-20 1088-1115 BL00477C 15.70 6.667e-17 291-308 BL00477B 9.05 7.207e-15 264-277 BL00477H 9.07 1.333e-14 1057-1069 BL00477D 12.73 2.059e-14 784-794
1717	BL01177	Anaphylatoxin domain proteins.	BL01177E 20.64 9.438e-12 845-872
1718	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 8.594e-35 151-199 BL00232B 32.79 5.579e-22 417-465 BL00232A 27.72 1.000e-20 57-90 BL00232C 10.65 3.613e-14 415-433 BL00232B 32.79 4.872e-11 534-582
1718	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 4.545e-15 415-433 PR00205A 14.73 5.600e-09 183-199
1718	BL00422	Granins proteins.	BL00422C 16.18 3.647e-09 226-254 BL00422C 16.18 9.294e-09 220-248
1718	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 2.256e-09 221-256 PF01140D 15.54 3.198e-09 217-252 PF01140D 15.54 9.791e-09 220-255
1722	BL00086	Cytochrome P450 cysteine heme-iron ligand proteins.	BL00086 20.87 8.714e-20 469-501
1722	PR00463	E-CLASS P450 GROUP I SIGNATURE	PR00463H 12.41 5.821e-10 469-480
1722	PR00408	MITOCHONDRIAL P450 SIGNATURE	PR00408F 11.33 6.000e-10 388-407
1722	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464I 14.64 1.771e-13 479-503 PR00464E 18.28 9.617e-11 389-410 PR00464C 18.84 1.000e-10 330-359 PR00464H 13.32 3.596e-09 466-480
1722	PR00465	E-CLASS P450 GROUP IV SIGNATURE	PR00465C 21.23 5.125e-25 332-359 PR00465H 17.76 5.500e-22 479-498 PR00465G 13.06 1.281e-17 463-480 PR00465D 14.64 2.607e-17 390-407 PR00465F 13.37 6.000e-15 439-458 PR00465E 15.03 9.217e-15 423-

Table 3A
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SEQ ID	Database entry ID	Description	Results*
			438 PR00465B 16.84 4.908e-09 113-137
1722	PR00385	P450 SUPERFAMILY SIGNATURE	PR00385D 13.11 1.667e-09 470-480 PR00385C 16.94 4.682e-09 395-407 PR00385A 14.97 5.865e-09 341-359 PR00385E 12.66 7.000e-09 479-491
1725	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 7.158e-10 107-117
1727	PR00220	SYNAPTOPHYSIN/SYNAPTOPORIN FAMILY SIGNATURE	PR00220B 15.48 2.800e-31 47-73 PR00220C 11.05 9.000e-31 100-125 PR00220D 8.32 3.842e-30 132-156 PR00220A 10.93 1.857e-28 23-46 PR00220E 3.46 4.273e-24 199-218
1727	BL00604	Synaptophysin / synaptoporin proteins.	BL00604A 9.13 1.000e-40 26-81 BL00604C 14.66 1.000e-40 117-149 BL00604D 12.28 1.000e-40 149-184 BL00604E 8.32 1.000e-40 184-226 BL00604F 5.96 1.000e-40 231-276 BL00604B 9.95 2.895e-37 87-117 BL00604F 5.96 1.122e-09 263-308
1727	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761A 5.81 3.662e-09 287-304
1727	BL00291	Prion protein.	BL00291A 4.49 8.138e-09 236-271
1728	BL00795	Involucrin proteins.	BL00795C 17.06 6.700e-09 159-204
1729	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747E 15.13 8.269e-18 225-243 PR00747H 12.76 5.610e-17 326-347 PR00747C 12.06 4.797e-11 145-164
1730	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209C 4.56 3.893e-09 77-91
1731	PR00244	NEUROKININ RECEPTOR SIGNATURE	PR00244H 13.12 9.357e-26 294-313 PR00244G 11.10 2.286e-15 268-280 PR00244F 10.47 3.132e-15 204-218 PR00244A 10.34 3.368e-15 29-41 PR00244B 12.45 1.000e-13 55-65 PR00244D 6.84 1.964e-13 125-136 PR00244C 13.44 3.118e-12 108-119 PR00244E 5.93 8.875e-12 183-193
1731	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237G 19.63 9.053e-19 275-302 PR00237F 13.57 5.800e-18 234-259 PR00237B 13.50 9.400e-17 68-90 PR00237A 11.48 5.765e-14 35-60 PR00237D 8.94 2.350e-11 133-155 PR00237E 13.03 1.600e-10 184-208
1731	BL00237	G-protein coupled receptors proteins.	BL00237C 13.19 2.688e-19 229-256 BL00237D 11.23 4.429e-13 285-302 BL00237B 5.28 5.909e-09 192-204
1732	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870D 15.74 8.755e-09 223-258
1733	BL00523	Sulfatases proteins.	BL00523A 13.36 8.800e-13 44-61

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SEQ ID	Database entry ID	Description	Results*
1734	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464A 20.47 9.719e-13 167-188
1735	BL00414	Profilin proteins.	BL00414D 15.59 5.909e-10 1037-1064
1735	PR00392	PROFILIN SIGNATURE	PR00392C 18.98 5.592e-10 986-1007 PR00392D 12.00 7.652e-09 1008-1023
1738	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003C 7.69 9.357e-09 73-83
1741	PR00915	LUTEOVIRUS GROUP 1 COAT PROTEIN SIGNATURE	PR00915G 15.24 6.875e-10 303-325
1745	PR00837	ALLERGEN V5/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 6.143e-20 126-143 PR00837A 14.77 1.973e-13 57-76
1745	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009D 14.19 4.300e-20 127-148 BL01009A 13.75 6.586e-13 57-75
1745	PR00838	VENOM ALLERGEN 5 SIGNATURE	PR00838G 16.07 2.033e-17 125-145 PR00838D 8.73 4.214e-09 57-76
1748	PR00920	SPUMAVIRUS ASPARTIC PROTEASE (A9) SIGNATURE	PR00920C 13.24 7.310e-09 212-234
1749	PR00672	INHIBIN BETA C CHAIN SIGNATURE	PR00672D 10.52 6.400e-09 96-113
1749	PD01572	PHOTOSYSTEM II REACTION CENTRE T PROTEIN PHOTOS.	PD01572 8.77 6.917e-09 544-574
1751	BL00713	Sodium:dicarboxylate symporter family proteins.	BL00713A 20.35 2.227e-35 314-356 BL00713B 13.04 8.000e-22 375-395
1751	PR00173	GLUTAMATE-ASPARTATE SYMPORTER SIGNATURE	PR00173C 13.89 7.353e-25 327-353 PR00173B 9.62 9.053e-13 19-40
1752	PR00219	SYNAPTOBREVIN SIGNATURE	PR00219C 9.04 7.750e-09 1-21
1753	PR00379	INTEIN SIGNATURE	PR00379A 16.17 9.780e-09 393-407
1757	PF00783	Inositol polyphosphate phosphatase, catalytic domain proteins homologue.	PF00783A 11.91 3.400e-14 539-549
1758	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169B 14.43 2.800e-30 239-268 PR00169C 16.31 3.109e-11 307-331
1762	BL00456	Sodium:solute symporter family proteins.	BL00456A 22.59 1.000e-40 16-71 BL00456C 24.55 1.000e-40 154-209 BL00456B 18.94 7.158e-28 92-122 BL00456D 6.92 2.862e-09 450-460
1763	DM01253	BNR MOTIF REPEAT.	DM01253A 11.72 7.785e-09 454-470
1763	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.200e-12 86-100 PR00019B 11.36 6.400e-10 83-97 PR00019A 11.19 2.333e-09 278-292 PR00019B 11.36 4.960e-09 275-289 PR00019A 11.19 9.333e-09 62-76
1764	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 5.714e-14 421-449
1765	PR00824	HEPATIC LIPASE SIGNATURE	PR00824A 7.81 7.214e-22 6-25
1768	BL00979	G-protein coupled receptors family 3	BL00979A 19.66 1.000e-40 77-125

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SEQ ID	Database entry ID	Description	Results*
		proteins.	
1769	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e-12 410-436
1769	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 5.345e-12 292-306 PR00360B 13.61 1.000e-11 427-441 PR00360A 14.59 2.895e-09 398-411
1769	PR00399	SYNAPTOTAGMIN SIGNATURE	PR00399B 14.27 8.425e-12 385-399 PR00399D 14.48 7.796e-09 328-339
1771	BL00312	Glycophorin A proteins.	BL00312B 9.22 5.781e-10 717-746
1771	BL00446	RNA polymerases D / 30 to 40 Kd subunits proteins.	BL00446C 18.90 9.087e-09 1326-1353
1771	PR00122	VACUOLAR ATP SYNTHASE 16 KD SUBUNIT SIGNATURE	PR00122D 9.97 9.330e-09 716-740
1771	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.745e-10 225-243 PR00205B 11.39 4.966e-09 333-351 PR00205B 11.39 9.390e-09 441-459
1771	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.308e-18 227-275 BL00232B 32.79 9.206e-17 443-491 BL00232B 32.79 3.407e-11 118-166 BL00232C 10.65 4.115e-10 225-243 BL00232C 10.65 4.462e-10 546-564 BL00232C 10.65 7.404e-10 333-351 BL00232C 10.65 9.842e-09 441-459
1773	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354Z 9.06 1.000e-16 102-151
1774	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE	PR00259C 16.40 5.313e-17 513-542 PR00259B 14.81 4.000e-14 486-513 PR00259D 13.50 2.340e-13 676-703
1774	BL00421	Transmembrane 4 family proteins.	BL00421B 17.62 1.000e-27 492-531 BL00421E 20.97 6.211e-13 673-703
1775	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245C 7.84 8.258e-17 319-335 PR00245A 18.03 9.265e-16 52-74 PR00245B 10.38 6.143e-14 258-273
1775	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 5.974e-12 83-123 BL00237A 27.68 5.974e-12 171-211
1775	PR00534	MELANOCORTIN RECEPTOR FAMILY SIGNATURE	PR00534A 11.49 6.123e-10 44-57
1775	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 9.333e-11 280-304 PR00237A 11.48 5.935e-09 19-44
1778	BL00417	Synaptobrevin proteins.	BL00417B 18.48 2.414e-19 141-195 BL00417A 7.74 6.704e-13 113-141
1778	PR00219	SYNAPTOSOMAL SIGNATURE	PR00219A 8.98 9.156e-13 118-138
1780	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.385e-15 255-273 BL00290A 20.89 1.529e-14 34-57 BL00290A 20.89 6.684e-13

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SEQ ID	Database entry ID	Description	Results*
			198-221
1782	BL00211	ABC transporters family proteins.	BL00211B 13.37 2.385e-17 558-590
1782	BL00674	AAA-protein family proteins.	BL00674B 4.46 5.622e-09 448-470
1782	PR00671	INHIBIN BETA B CHAIN SIGNATURE	PR00671B 4.29 9.408e-09 396-416
1782	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 9.649e-09 451-470
1783	PR00176	SODIUM/NEUROTRANSMITTER SYMPORTER SIGNATURE	PR00176C 10.84 8.615e-25 283-310 PR00176A 16.82 5.909e-24 211-233 PR00176B 7.31 4.600e-23 240-260 PR00176D 9.02 6.143e-21 412-430 PR00176F 10.73 1.333e-20 548-568 PR00176E 11.41 2.227e-20 494-515 PR00176G 12.48 5.034e-17 630-651 PR00176H 15.27 7.429e-17 670-691
1783	BL00610	Sodium:neurotransmitter symporter family proteins.	BL00610A 17.73 1.000e-40 211-261 BL00610B 23.65 1.000e-40 274-324 BL00610D 20.97 1.000e-40 451-504 BL00610F 29.02 1.000e-40 641-696 BL00610E 20.34 9.100e-37 544-587 BL00610G 12.89 6.087e-22 700-723 BL00610C 12.94 4.282e-15 385-437
1784	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 7.592e-09 799-842
1785	BL00349	CTF/NF-I proteins.	BL00349A 10.07 1.000e-40 649-695 BL00349C 9.33 1.000e-40 723-766 BL00349E 10.79 9.833e-36 793-836 BL00349B 10.51 1.205e-34 695-723 BL00349D 11.70 1.000e-33 766-793
1786	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.100e-11 243-257 PR00019B 11.36 9.100e-10 431-445 PR00019A 11.19 2.000e-09 434-448 PR00019A 11.19 4.667e-09 482-496 PR00019B 11.36 6.040e-09 643-657 PR00019B 11.36 6.400e-09 597-611 PR00019B 11.36 9.640e-09 479-493
1789	PR00702	ACRIFLAVIN RESISTANCE PROTEIN FAMILY SIGNATURE	PR00702G 9.63 4.214e-22 74-98 PR00702F 12.14 1.474e-19 49-73 PR00702H 12.94 7.955e-17 153-171 PR00702I 17.85 7.857e-16 216-231
1790	DM00914	BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEMS INNER MEMBRANE.	DM00914C 21.08 8.457e-35 121-168 DM00914B 22.92 5.750e-30 45-86
1790	PR00797	STREPTOPAIN (C10) CYSTEINE PROTEASE FAMILY SIGNATURE	PR00797F 12.40 9.804e-09 41-63
1791	BL00942	glpT family of transporters proteins.	BL00942E 21.14 9.700e-40 104-

Table 3A
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SEQ ID	Database entry ID	Description	Results*
			145 BL00942D 18.76 1.273e-31 55-92 BL00942C 14.04 2.688e-21 13-33 BL00942F 15.07 7.632e-21 162-180
1792	BL00523	Sulfatases proteins.	BL00523C 12.64 5.800e-12 593-604
1796	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 7.261e-10 315-329 PR00019B 11.36 4.600e-09 312-326
1798	PR00303	PREPROTEIN TRANSLOCASE SECY SUBUNIT SIGNATURE	PR00303E 14.69 1.429e-22 98-122 PR00303D 16.15 8.650e-22 72-98 PR00303C 15.93 9.036e-19 34-58
1798	BL00755	Protein secY proteins.	BL00755C 14.21 2.500e-18 89-105
1798	PR00825	VESPID VENOM ALLERGEN PHOSPHOLIPASE A1 SIGNATURE	PR00825B 14.81 9.738e-09 234-255
1800	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081A 10.53 1.439e-11 179-197
1800	PR00669	INHIBIN ALPHA CHAIN SIGNATURE	PR00669B 8.27 2.976e-09 80-97
1801	BL01022	PTR2 family proton/oligopeptide symporters proteins.	BL01022E 23.51 1.173e-12 474-510 BL01022D 9.42 3.455e-11 12-25
1802	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 2.350e-14 489-505
1802	PR00792	PEPSIN (A1) ASPARTIC PROTEASE FAMILY SIGNATURE	PR00792B 12.78 7.750e-14 331-345 PR00792C 9.10 1.000e-12 380-392
1802	BL00141	Eukaryotic and viral aspartyl proteases proteins.	BL00141C 9.74 1.000e-11 336-346 BL00141D 6.28 3.700e-11 380-390
1802	BL01177	Anaphylatoxin domain proteins.	BL01177C 17.39 8.780e-10 483-502
1804	PR00165	ANION EXCHANGER SIGNATURE	PR00165F 10.39 9.667e-12 32-51
1804	BL00219	Anion exchangers family proteins.	BL00219L 18.71 1.000e-40 126-165 BL00219N 10.66 6.164e-31 194-238 BL00219M 9.98 3.100e-17 148-194 BL00219P 19.59 6.123e-13 247-274 BL00219H 10.06 4.555e-11 11-59 BL00219K 12.73 8.780e-10 84-126
1805	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 3.118e-16 786-804 BL00972D 22.55 1.500e-14 1281-1306 BL00972E 20.72 6.850e-13 1308-1330 BL00972B 9.45 7.923e-10 882-892
1810	BL00216	Sugar transport proteins.	BL00216B 27.64 8.531e-13 736-786
1810	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973A 21.17 1.391e-11 708-745
1813	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.308e-15 288-301
1813	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048B 6.02 7.188e-10 285-295 PR00048A 10.52 8.043e-10 269-283 PR00048A 10.52 3.880e-09 297-311
1813	BL00028	Zinc finger, C2H2 type, domain	BL00028 16.07 1.692e-11 515-532

Table 3A
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SEQ ID	Database entry ID	Description	Results*
		proteins.	BL00028 16.07 4.000e-10 487-504 BL00028 16.07 1.257e-09 773-790 BL00028 16.07 5.371e-09 272-289
1813	PF01059	NADH-ubiquinone oxidoreductase chain 4, amino terminus.	PF01059A 13.84 6.192e-09 19-53
1815	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134B 15.99 8.560e-17 316-340 BL00134A 11.96 4.214e-16 53-70
1815	BL00495	Apple domain proteins.	BL00495M 8.50 5.071e-16 226-261 BL00495N 11.04 4.438e-15 308-343
1815	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722A 12.27 4.414e-14 54-70 PR00722C 10.87 9.471e-13 315-328
1815	BL00021	Kringle domain proteins.	BL00021B 13.33 6.580e-16 53-71 BL00021C 22.21 2.125e-10 235-257
1815	BL01253	Type I fibronectin domain proteins.	BL01253G 11.34 4.316e-12 315-329 BL01253E 16.01 9.899e-11 224-261 BL01253D 4.84 5.920e-09 53-67
1815	PR00839	V8 SERINE PROTEASE FAMILY SIGNATURE	PR00839B 11.20 6.425e-09 53-71
1816	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354H 18.00 5.618e-12 134-174
1817	BL00859	GTP cyclohydrolase I proteins.	BL00859B 13.15 9.057e-09 72-113
1819	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 2.421e-20 1431-1450 PR00700C 13.17 5.765e-17 1390-1408 PR00700F 11.18 7.429e-12 1478-1489
1819	PR00213	MYELIN P0 PROTEIN SIGNATURE	PR00213E 5.51 1.656e-09 1186-1211
1819	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 1.000e-14 1434-1445 BL00383D 11.92 1.692e-14 1394-1407 BL00383A 13.34 6.850e-14 1280-1295 BL00383F 15.51 4.240e-13 1472-1488 BL00383C 10.10 6.625e-10 1318-1329 BL00383B 7.61 4.000e-09 1305-1314
1819	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 1.450e-10 688-707 PR00014C 15.44 6.400e-10 866-885 PR00014C 15.44 2.565e-09 510-529 PR00014C 15.44 5.696e-09 1056-1075
1821	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245C 7.84 4.073e-15 361-377 PR00245E 12.40 8.286e-12 414-429
1821	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237G 19.63 5.814e-09 395-422
1822	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242F 12.18 8.522e-09 322-344

* Results include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
912	IPB001398A	Macrophage migration inhibitory factor family	23.60 6.73e-29 124-163
912	IPB001398B	Macrophage migration inhibitory factor family	19.16 2.06e-20 164-190
912	IPB001398C	Macrophage migration inhibitory factor family	26.46 6.96e-11 192-238
913	IPB000033A	Low-density lipoprotein (ldl) receptor, YWTD repeat	21.82 4.35e-09 514-536
913	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 4.48e-10 817-827
913	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 7.10e-10 574-584
913	IPB000118B	Granulin	7.94 9.20e-09 472-510
913	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 1.96e-11 484-499
913	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 3.84e-14 696-711
913	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 3.86e-13 569-584
913	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 6.54e-17 812-827
913	IPB000561	EGF-like domain	4.89 3.57e-09 821-829
913	IPB001862A	Membrane attack complex components/perforin/complement C9	12.54 8.02e-10 175-190
913	IPB001881B	Calcium-binding EGF-like domain	12.28 4.79e-11 696-707
913	IPB001881B	Calcium-binding EGF-like domain	12.28 5.20e-12 812-823
913	IPB001881B	Calcium-binding EGF-like domain	12.28 8.58e-11 527-538
913	IPB001881B	Calcium-binding EGF-like domain	12.28 8.71e-10 569-580
913	IPB001881B	Calcium-binding EGF-like domain	12.28 9.53e-11 484-495
913	IPB002861B	Reeler domain	10.50 4.48e-09 124-152
913	IPB002861B	Reeler domain	10.50 8.98e-09 181-209
913	IPB002861C	Reeler domain	23.17 6.48e-09 111-165
913	IPB003367A	Thrombospondin type 3 repeat	11.78 5.13e-09 782-802
913	IPB003367A	Thrombospondin type 3 repeat	11.78 5.83e-10 577-597
913	IPB003886D	Extracellular domain in nidogen	13.91 3.49e-09 569-588
913	IPB003886D	Extracellular domain in nidogen	13.91 4.78e-13 696-715
913	IPB003886D	Extracellular domain in nidogen	13.91 9.41e-10 812-831
913	PR00010C	Type II EGF-like signature III	6.98 3.63e-09 574-584
913	PR00010C	Type II EGF-like signature III	6.98 8.02e-09 701-711
913	PR00010C	Type II EGF-like signature III	6.98 9.47e-13 817-827
913	PR00907B	Thrombomodulin signature II	11.50 9.43e-09 808-824
913	PR00907G	Thrombomodulin signature VII	10.43 8.09e-10 812-838
913	PR00907G	Thrombomodulin signature VII	10.43 8.85e-10 696-722
913	PR00907G	Thrombomodulin signature VII	10.43 9.27e-09 569-595
913	PR01303D	Plasmodium circumsporozoite protein signature IV	10.57 2.00e-09 187-204
914	IPB001398A	Macrophage migration inhibitory factor family	23.60 9.76e-26 2-41
914	IPB001398B	Macrophage migration inhibitory factor family	19.16 6.31e-18 42-68
914	IPB001398C	Macrophage migration inhibitory factor family	26.46 5.14e-12 70-116
915	IPB001398A	Macrophage migration inhibitory factor family	23.60 3.25e-20 2-41

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
915	IPB001398B	Macrophage migration inhibitory factor family	19.16 2.06e-20 55-81
915	IPB001398C	Macrophage migration inhibitory factor family	26.46 7.39e-36 83-129
916	IPB000001B	Kringle	18.04 8.09e-19 286-310
916	IPB000001C	Kringle	20.41 2.23e-22 331-351
916	IPB000001D	Kringle	11.31 3.61e-17 469-485
916	IPB000001E	Kringle	16.02 8.58e-13 544-557
916	IPB000001F	Kringle	10.14 7.65e-11 567-577
916	IPB000001G	Kringle	29.29 2.80e-16 588-616
916	IPB000001H	Kringle	12.24 3.45e-13 628-638
916	IPB000177M	Apple domain	9.18 4.82e-10 545-579
916	IPB000177N	Apple domain	10.17 3.25e-20 618-652
916	IPB000177O	Apple domain	14.39 6.13e-17 653-681
916	IPB000561	EGF-like domain	4.89 4.21e-09 267-275
916	IPB000562	Type II fibronectin collagen-binding domain	10.39 9.05e-20 132-148
916	IPB001254A	Serine proteases, trypsin family	9.98 6.09e-14 469-485
916	IPB001254B	Serine proteases, trypsin family	15.01 3.50e-17 626-649
916	IPB001254C	Serine proteases, trypsin family	16.54 1.00e-18 656-675
916	IPB001774D	Delta serrate ligand	19.23 5.82e-09 152-198
916	IPB001881A	Calcium-binding EGF-like domain	8.72 1.00e-08 245-254
916	IPB001881A	Calcium-binding EGF-like domain	8.72 8.20e-09 164-173
916	PR00010A	Type II EGF-like signature I	12.91 6.54e-10 160-171
916	PR00011B	Type III EGF-like signature II	13.08 6.42e-09 179-197
916	PR00011B	Type III EGF-like signature II	13.08 9.38e-09 260-278
916	PR00013A	Fibronectin type II repeat signature I	12.70 4.60e-10 105-114
916	PR00013B	Fibronectin type II repeat signature II	11.78 5.25e-10 116-128
916	PR00013C	Fibronectin type II repeat signature III	12.27 9.47e-19 132-147
916	PR00018A	Kringle domain signature I	12.23 8.84e-12 286-301
916	PR00018B	Kringle domain signature II	16.62 1.75e-09 302-314
916	PR00018C	Kringle domain signature III	16.77 7.00e-21 331-351
916	PR00018D	Kringle domain signature IV	12.83 9.04e-10 356-367
916	PR00722A	Chymotrypsin serine protease family (S1) signature I	12.06 9.36e-14 470-485
916	PR00722C	Chymotrypsin serine protease family (S1) signature III	10.74 8.62e-14 625-637
916	PR01236A	Tumour necrosis factor beta (lymphotoxin-alpha) signature I	4.92 8.22e-09 22-38
917	IPB000034A	Laminin B	22.21 3.69e-10 419-454
917	IPB000034A	Laminin B	22.21 7.22e-13 1046-1081
917	IPB000034A	Laminin B	22.21 9.42e-10 291-326
917	IPB000034B	Laminin B	21.22 8.38e-11 808-846
917	IPB000034B	Laminin B	21.22 9.07e-19 443-481
917	IPB000034C	Laminin B	12.97 1.12e-10 542-560
917	IPB000034C	Laminin B	12.97 2.29e-09 805-823
917	IPB000034C	Laminin B	12.97 3.10e-10 492-510
917	IPB000034C	Laminin B	12.97 5.09e-09 897-915
917	IPB000034C	Laminin B	12.97 5.29e-12 1067-1085
917	IPB000034C	Laminin B	12.97 8.17e-14 955-973
917	IPB000034C	Laminin B	12.97 8.43e-11 853-871
917	IPB000034C	Laminin B	12.97 8.62e-12 1114-1132
917	IPB001134C	Netrin, C-terminus	17.82 9.77e-09 1014-1028
917	IPB001774C	Delta serrate ligand	18.25 9.27e-09 1105-1147

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
917	IPB001886A	Laminin N-terminal (Domain VI)	8.51 9.44e-10 119-126
917	IPB001886B	Laminin N-terminal (Domain VI)	15.20 4.81e-24 269-291
917	IPB001886C	Laminin N-terminal (Domain VI)	24.54 2.14e-13 377-416
917	IPB001886C	Laminin N-terminal (Domain VI)	24.54 6.21e-11 1009-1048
917	IPB001886C	Laminin N-terminal (Domain VI)	24.54 6.55e-12 1067-1106
917	IPB001886C	Laminin N-terminal (Domain VI)	24.54 7.04e-11 955-994
917	IPB001886C	Laminin N-terminal (Domain VI)	24.54 8.03e-12 440-479
917	IPB001886C	Laminin N-terminal (Domain VI)	24.54 8.41e-32 312-351
917	IPB001886C	Laminin N-terminal (Domain VI)	24.54 8.81e-09 853-892
917	IPB001886D	Laminin N-terminal (Domain VI)	12.51 3.39e-13 893-911
917	IPB001886D	Laminin N-terminal (Domain VI)	12.51 5.86e-09 308-326
917	IPB001886D	Laminin N-terminal (Domain VI)	12.51 7.20e-14 1005-1023
917	IPB001886D	Laminin N-terminal (Domain VI)	12.51 9.64e-20 373-391
917	IPB001886E	Laminin N-terminal (Domain VI)	10.90 1.55e-11 438-454
917	IPB001886E	Laminin N-terminal (Domain VI)	10.90 2.20e-12 1065-1081
917	IPB001886E	Laminin N-terminal (Domain VI)	10.90 3.02e-11 490-506
917	IPB001886E	Laminin N-terminal (Domain VI)	10.90 6.00e-12 851-867
917	IPB001886E	Laminin N-terminal (Domain VI)	10.90 6.14e-15 540-556
917	IPB001886E	Laminin N-terminal (Domain VI)	10.90 6.33e-11 1112-1128
917	IPB001886E	Laminin N-terminal (Domain VI)	10.90 7.43e-11 310-326
917	IPB001886E	Laminin N-terminal (Domain VI)	10.90 9.07e-17 803-819
917	IPB003884C	Factor I membrane attack complex	13.00 3.35e-09 411-429
917	IPB003884C	Factor I membrane attack complex	13.00 3.87e-09 833-851
917	IPB003888L	FY-rich domain N-terminus	21.19 8.82e-10 339-385
917	PR00011A	Type III EGF-like signature I	14.05 2.02e-14 485-503
917	PR00011A	Type III EGF-like signature I	14.05 2.76e-17 1060-1078
917	PR00011A	Type III EGF-like signature I	14.05 3.35e-11 433-451
917	PR00011A	Type III EGF-like signature I	14.05 4.41e-13 798-816
917	PR00011A	Type III EGF-like signature I	14.05 4.72e-16 535-553
917	PR00011A	Type III EGF-like signature I	14.05 7.30e-15 846-864
917	PR00011A	Type III EGF-like signature I	14.05 7.50e-09 305-323
917	PR00011A	Type III EGF-like signature I	14.05 8.24e-16 1107-1125
917	PR00011B	Type III EGF-like signature II	13.08 4.17e-14 485-503
917	PR00011B	Type III EGF-like signature II	13.08 4.35e-15 1107-1125
917	PR00011B	Type III EGF-like signature II	13.08 4.86e-17 846-864
917	PR00011B	Type III EGF-like signature II	13.08 6.46e-12 798-816
917	PR00011B	Type III EGF-like signature II	13.08 6.96e-10 433-451
917	PR00011B	Type III EGF-like signature II	13.08 7.71e-15 535-553
917	PR00011B	Type III EGF-like signature II	13.08 8.00e-14 1060-1078
917	PR00011C	Type III EGF-like signature III	25.79 1.15e-09 455-483
917	PR00011C	Type III EGF-like signature III	25.79 6.21e-10 440-468
917	PR00011C	Type III EGF-like signature III	25.79 9.82e-12 817-845
917	PR00011D	Type III EGF-like signature IV	12.12 1.00e-16 1107-1125
917	PR00011D	Type III EGF-like signature IV	12.12 2.62e-14 846-864
917	PR00011D	Type III EGF-like signature IV	12.12 3.00e-13 535-553
917	PR00011D	Type III EGF-like signature IV	12.12 5.00e-13 485-503
917	PR00011D	Type III EGF-like signature IV	12.12 5.50e-14 1060-1078
917	PR00011D	Type III EGF-like signature IV	12.12 6.23e-11 433-451
917	PR00011D	Type III EGF-like signature IV	12.12 7.98e-12 798-816
918	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 1.00e-09 304-314
918	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 1.00e-10 132-142

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SEQ ID NO:	Database entry ID	Description	Results*
918	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 4.19e-10 344-354
918	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 5.74e-09 384-394
918	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 7.97e-10 91-101
918	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 3.12e-15 379-394
918	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 3.37e-14 299-314
918	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 3.45e-13 46-61
918	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 5.76e-15 339-354
918	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 7.55e-13 127-142
918	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 8.77e-13 86-101
918	IPB000561	EGF-like domain	4.89 5.50e-09 55-63
918	IPB000859	CUB domain	19.99 7.67e-17 721-756
918	IPB001881B	Calcium-binding EGF-like domain	12.28 1.47e-11 127-138
918	IPB001881B	Calcium-binding EGF-like domain	12.28 1.47e-11 299-310
918	IPB001881B	Calcium-binding EGF-like domain	12.28 5.00e-14 379-390
918	IPB001881B	Calcium-binding EGF-like domain	12.28 5.26e-11 86-97
918	IPB001881B	Calcium-binding EGF-like domain	12.28 7.00e-13 339-350
918	IPB001881B	Calcium-binding EGF-like domain	12.28 8.71e-10 46-57
918	IPB002557B	Chitin binding domain	12.64 3.08e-09 653-666
918	IPB003367A	Thrombospondin type 3 repeat	11.78 7.62e-14 54-74
918	IPB003886D	Extracellular domain in nidogen	13.91 1.54e-13 46-65
918	IPB003886D	Extracellular domain in nidogen	13.91 2.13e-11 339-358
918	IPB003886D	Extracellular domain in nidogen	13.91 9.17e-09 379-398
918	PR00010C	Type II EGF-like signature III	6.98 4.48e-10 132-142
918	PR00010C	Type II EGF-like signature III	6.98 5.61e-09 304-314
918	PR00010C	Type II EGF-like signature III	6.98 5.83e-09 384-394
918	PR00010C	Type II EGF-like signature III	6.98 6.05e-09 51-61
918	PR00010C	Type II EGF-like signature III	6.98 8.02e-09 91-101
918	PR00907B	Thrombomodulin signature II	11.50 9.16e-10 215-231
918	PR00907G	Thrombomodulin signature VII	10.43 6.84e-10 46-72
918	PR00907G	Thrombomodulin signature VII	10.43 7.51e-10 379-405
919	IPB001415A	Parathyroid hormone family	18.60 2.50e-37 80-114
919	IPB001415B	Parathyroid hormone family	26.47 1.00e-40 133-181
920	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 5.32e-11 144-154
920	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 6.76e-11 103-113
920	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 8.92e-11 17-27
920	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 3.05e-13 139-154
920	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 5.26e-14 12-27
920	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 9.59e-13 98-113
920	IPB000561	EGF-like domain	4.89 1.00e-09 252-260

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SEQ ID NO:	Database entry ID	Description	Results*
920	IPB000561	EGF-like domain	4.89 1.00e-09 67-75
920	IPB001881B	Calcium-binding EGF-like domain	12.28 1.43e-10 12-23
920	IPB001881B	Calcium-binding EGF-like domain	12.28 6.57e-10 139-150
920	IPB001881B	Calcium-binding EGF-like domain	12.28 7.86e-10 98-109
920	PR00010C	Type II EGF-like signature III	6.98 3.63e-09 103-113
920	PR00010C	Type II EGF-like signature III	6.98 7.59e-09 144-154
920	PR00011A	Type III EGF-like signature I	14.05 3.50e-09 331-349
920	PR00011A	Type III EGF-like signature I	14.05 6.09e-14 288-306
920	PR00011A	Type III EGF-like signature I	14.05 7.90e-12 376-394
920	PR00011B	Type III EGF-like signature II	13.08 1.00e-13 288-306
920	PR00011B	Type III EGF-like signature II	13.08 3.36e-12 376-394
920	PR00011B	Type III EGF-like signature II	13.08 3.59e-09 331-349
920	PR00011D	Type III EGF-like signature IV	12.12 2.50e-13 376-394
920	PR00011D	Type III EGF-like signature IV	12.12 2.86e-12 288-306
920	PR00011D	Type III EGF-like signature IV	12.12 4.05e-11 331-349
920	PR00764F	Complement C9 signature VI	15.74 5.10e-09 236-256
920	PR00907B	Thrombomodulin signature II	11.50 8.32e-10 54-70
921	IPB000827A	Small cytokines (intercrine/chemokine), C-C subfamily	8.72 5.24e-11 35-45
922	IPB000834A	Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family	18.14 1.77e-11 167-188
922	IPB000834B	Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family	13.51 5.50e-14 201-215
922	IPB000834C	Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family	17.20 6.66e-12 270-286
922	IPB000834D	Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family	18.95 3.25e-23 297-323
922	IPB000834E	Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family	9.80 3.33e-13 325-339
922	IPB000834F	Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family	12.40 9.18e-09 382-394
922	IPB000834G	Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family	14.46 6.00e-15 415-430
922	PR00765B	Carboxypeptidase A metalloprotease (M14) family signature II	14.48 8.04e-15 197-211
922	PR00765C	Carboxypeptidase A metalloprotease (M14) family signature III	10.88 5.50e-09 277-285
922	PR00765D	Carboxypeptidase A metalloprotease (M14) family signature IV	14.06 4.91e-14 330-343
923	IPB002181A	Fibrinogen beta and gamma chains C-terminal globular domain	18.44 7.00e-11 64-80
923	IPB002181B	Fibrinogen beta and gamma chains C-terminal globular domain	20.16 4.86e-32 93-129
923	IPB002181C	Fibrinogen beta and gamma chains C-terminal globular domain	15.87 6.88e-13 134-146
923	IPB002181D	Fibrinogen beta and gamma chains C-terminal globular domain	29.18 1.23e-18 153-193
923	IPB002181E	Fibrinogen beta and gamma chains C-terminal globular domain	27.75 9.71e-23 205-237
927	IPB000774B	Domain amino terminal to FKBP-type peptidyl-prolyl isomerase	11.42 1.29e-12 54-81
927	IPB000774C	Domain amino terminal to FKBP-type peptidyl-prolyl isomerase	10.28 7.46e-19 84-113
927	IPB001179	FKBP-type peptidyl-prolyl cis-trans	22.74 4.60e-26 80-113

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
		isomerase (PPIase)	
932	IPB001359H	Synapsin	22.58 6.66e-10 176-226
936	PR00436A	Interleukin-8 signature I	15.20 8.23e-09 3-26
937	IPB000308B	14-3-3 proteins	12.24 2.33e-40 77-116
937	IPB000308C	14-3-3 proteins	18.31 1.00e-36 143-192
937	IPB000308D	14-3-3 proteins	12.57 1.69e-35 215-269
937	PR00305A	14-3-3 protein zeta signature I	9.70 9.18e-33 77-106
937	PR00305B	14-3-3 protein zeta signature II	11.03 4.52e-22 126-150
937	PR00305C	14-3-3 protein zeta signature III	9.89 5.50e-28 159-181
937	PR00305D	14-3-3 protein zeta signature IV	17.40 4.81e-27 194-220
937	PR00305F	14-3-3 protein zeta signature VI	15.40 1.00e-36 248-277
938	IPB002048	EF-hand family	7.91 5.24e-10 123-135
939	PR01353A	Glucagon family receptor signature I	8.87 4.86e-10 5-18
940	IPB001875B	Death effector domain	13.21 1.00e-08 500-509
940	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 9.65e-09 182-219
940	IPB003530A	Long hematopoietin receptor, soluble alpha chains	23.64 8.76e-09 339-393
941	IPB000483	Leucine rich repeat C-terminal domain	11.18 8.11e-14 242-256
941	PR00019B	Leucine-rich repeat signature II	11.42 8.91e-09 135-148
941	PR00364D	Disease resistance protein signature IV	14.89 4.60e-09 84-100
944	IPB000215A	Serpins	13.01 9.31e-15 200-223
944	IPB000215B	Serpins	9.87 4.79e-12 296-308
944	IPB000215C	Serpins	13.90 5.18e-11 323-337
944	IPB000215D	Serpins	15.35 9.27e-11 430-456
944	IPB000215E	Serpins	15.36 1.00e-15 508-532
944	IPB000895A	Transthyretin precursor	12.60 4.04e-09 39-58
944	PR00743B	Glycosyl hydrolase family 36 signature II	14.95 8.83e-09 240-260
945	IPB002905C	N2,N2-dimethylguanosine tRNA methyltransferase	19.39 5.00e-11 115-136
947	IPB000306	FYVE Zn-finger, rabphilin/VPS27/FAB1 type	8.96 3.25e-18 552-564
947	IPB001841	RING finger	10.69 3.37e-09 559-568
950	IPB001304A	C-type lectin domain	17.98 5.50e-11 117-141
950	PR00356D	Type II antifreeze protein signature IV	12.93 7.41e-09 174-190
951	IPB001304A	C-type lectin domain	17.98 2.29e-15 202-226
951	PR00356A	Type II antifreeze protein signature I	13.29 6.70e-10 197-209
951	PR00356B	Type II antifreeze protein signature II	12.71 4.63e-10 209-226
953	IPB001359H	Synapsin	22.58 4.43e-10 16-66
953	PR00910A	Luteovirus ORF6 protein signature I	2.74 3.46e-09 107-119
954	PR00901H	Pheromone B alpha-1 receptor signature VIII	14.75 4.05e-09 56-66
955	PR00436A	Interleukin-8 signature I	15.20 4.39e-09 36-59
956	IPB003406B	Core-2/I-Branching enzyme	11.63 9.31e-37 94-128
956	IPB003406C	Core-2/I-Branching enzyme	11.36 7.26e-37 145-184
956	IPB003406D	Core-2/I-Branching enzyme	23.29 1.82e-33 191-230
956	IPB003406E	Core-2/I-Branching enzyme	22.75 3.87e-29 251-292
958	IPB000130	Neutral zinc metalloproteases, zinc-binding region	5.86 6.54e-11 236-246
958	IPB001818A	Matrixin	14.60 7.35e-28 88-117
958	IPB001818B	Matrixin	26.48 7.75e-39 136-177
958	IPB001818C	Matrixin	24.38 1.00e-40 180-225
958	IPB001818D	Matrixin	14.91 5.34e-30 230-261
958	IPB001818E	Matrixin	8.86 4.67e-13 269-282

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
958	IPB001818F	Matrixin	11.19 6.85e-22 305-325
958	IPB001818G	Matrixin	14.71 2.61e-12 342-354
958	IPB001818H	Matrixin	15.46 2.89e-28 408-434
958	IPB002870E	Reprolysin family propeptide	11.90 5.22e-10 238-250
958	PR00138A	Matrixin signature I	12.54 6.79e-16 108-121
958	PR00138B	Matrixin signature II	14.84 1.56e-17 155-170
958	PR00138C	Matrixin signature III	20.07 5.74e-28 178-206
958	PR00138D	Matrixin signature IV	14.57 7.86e-27 236-261
958	PR00138E	Matrixin signature V	7.10 4.96e-13 269-282
958	PR00480B	Astacin family signature II	14.35 4.32e-11 231-249
958	PR00997G	Fragilysin metalloproteinase (M10C) enterotoxin signature VII	11.64 8.53e-09 242-258
962	IPB000953	Chromo domain	14.73 2.29e-17 63-81
962	IPB003606E	N-terminal to some SET domains	9.57 2.89e-12 226-235
962	IPB003606G	N-terminal to some SET domains	13.63 4.00e-10 262-290
962	PR00504C	Chromodomain signature III	12.01 1.97e-10 72-84
965	IPB001729	Surfactant associated polypeptide SP-C palmitoylation sites	9.43 9.11e-09 19-52
967	IPB000276A	Rhodopsin-like GPCR superfamily	11.56 9.18e-09 118-129
967	IPB000276D	Rhodopsin-like GPCR superfamily	9.40 9.22e-10 229-245
967	IPB001133A	NADH-ubiquinone oxidoreductase chain 4L	13.73 5.50e-10 89-119
967	PR00237A	Rhodopsin-like GPCR superfamily signature I	9.81 8.31e-09 26-50
967	PR00245B	Olfactory receptor signature II	13.73 3.57e-09 129-141
967	PR00245D	Olfactory receptor signature IV	9.34 2.59e-13 183-192
967	PR00245E	Olfactory receptor signature V	8.96 5.15e-16 230-241
967	PR00534A	Melanocortin receptor family signature I	12.77 2.83e-09 51-63
968	IPB002328A	Zinc-containing alcohol dehydrogenase	20.74 6.65e-09 179-210
968	IPB002328B	Zinc-containing alcohol dehydrogenase	14.71 9.03e-12 223-248
968	IPB002364	Quinone oxidoreductase/zeta-crystallin	20.78 6.67e-12 223-250
970	IPB001017A	Dehydrogenase, E1 component	11.25 7.35e-13 126-138
970	IPB001017B	Dehydrogenase, E1 component	25.91 2.64e-27 152-184
970	IPB001017C	Dehydrogenase, E1 component	15.29 7.00e-22 200-219
970	IPB001017D	Dehydrogenase, E1 component	18.59 1.45e-40 256-294
970	IPB001017E	Dehydrogenase, E1 component	10.22 3.65e-15 312-325
970	IPB001017F	Dehydrogenase, E1 component	17.40 9.31e-23 340-360
975	PR01281D	Corticotropin releasing factor type 2 receptor signature IV	9.32 8.52e-09 388-403
977	PR00457A	Animal haem peroxidase signature I	15.27 6.79e-12 162-173
977	PR00457B	Animal haem peroxidase signature II	12.43 1.26e-15 216-231
977	PR00457C	Animal haem peroxidase signature III	18.81 1.51e-14 366-384
977	PR00457D	Animal haem peroxidase signature IV	18.35 5.50e-22 384-404
977	PR00457E	Animal haem peroxidase signature V	19.97 4.91e-26 409-435
977	PR00457F	Animal haem peroxidase signature VI	14.42 6.05e-10 461-471
977	PR00457G	Animal haem peroxidase signature VII	14.17 3.25e-18 590-610
977	PR00457H	Animal haem peroxidase signature VIII	14.82 6.19e-13 684-698
978	IPB001271	Mammalian defensin	19.97 6.36e-13 95-123
985	IPB001862A	Membrane attack complex components/perforin/complement C9	12.54 8.63e-10 145-160
985	IPB002174A	Furin-like cysteine rich region	30.51 9.03e-10 26-57
987	PR00019B	Leucine-rich repeat signature II	11.42 8.33e-10 124-137
987	PR00019B	Leucine-rich repeat signature II	11.42 8.33e-10 316-329
988	IPB000392A	NifH/frxC family	9.08 2.98e-11 107-122
988	IPB000808A	Mrp family	23.51 8.67e-37 101-145

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SEQ ID NO:	Database entry ID	Description	Results*
988	IPB000808B	Mrp family	15.70 7.48e-36 191-227
988	IPB000808C	Mrp family	23.57 8.77e-29 250-285
988	IPB000808D	Mrp family	28.05 6.40e-24 297-337
988	IPB001984C	ATP-dependent serine proteases, Lon family	12.76 9.82e-09 103-139
988	IPB003348A	Anion-transporting ATPase	20.06 7.75e-15 106-143
988	PR00091A	Nitrogenase component II signature I	7.81 4.38e-09 109-122
988	PR00094A	Adenylate kinase signature I	9.62 9.86e-09 107-120
988	PR00364A	Disease resistance protein signature I	8.29 7.59e-10 105-120
989	IPB001007B	von Willebrand factor, type C repeat	10.03 4.79e-09 259-268
989	IPB001846B	von Willebrand factor type D domain	10.86 1.82e-12 489-503
989	IPB002919B	Trypsin Inhibitor-like cysteine rich domain	21.14 6.45e-10 321-343
989	PR00163B	Rubredoxin signature II	15.17 9.25e-09 215-231
992	IPB000353B	Class II histocompatibility antigen, beta chain, beta-1 domain	19.16 8.48e-10 133-182
992	IPB003006A	Immunoglobulin and major histocompatibility complex domain	17.51 1.38e-11 154-176
994	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 6.48e-11 86-123
994	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 8.04e-11 267-304
995	IPB001283A	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	16.26 6.67e-10 29-48
995	IPB001283B	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	13.09 2.33e-12 57-72
995	IPB001283E	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	13.34 5.50e-20 127-147
995	IPB001283F	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	10.49 6.48e-11 160-170
995	IPB003106E	Homeobox associated leucine zipper	13.73 6.90e-09 25-55
995	PR00837A	Allergen V5/Tpx-1 family signature I	14.69 1.56e-14 57-75
995	PR00837C	Allergen V5/Tpx-1 family signature III	16.31 5.50e-20 126-142
995	PR00837D	Allergen V5/Tpx-1 family signature IV	11.13 3.70e-11 160-173
995	PR00838D	Venom allergen 5 signature IV	8.59 3.57e-09 57-75
995	PR00838G	Venom allergen 5 signature VII	15.39 8.60e-18 125-144
1000	IPB000353B	Class II histocompatibility antigen, beta chain, beta-1 domain	19.16 3.25e-13 21-70
1000	IPB001003B	MHC Class II, alpha chain, alpha-1 domain	14.72 8.38e-11 29-72
1000	IPB003006A	Immunoglobulin and major histocompatibility complex domain	17.51 3.63e-11 42-64
1000	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 8.31e-17 78-115
1002	IPB000306	FYVE Zn-finger, rabphilin/VPS27/FAB1 type	8.96 9.74e-09 181-193
1002	IPB000822	Zinc finger, C2H2 type	14.67 1.60e-16 213-238
1002	IPB000822	Zinc finger, C2H2 type	14.67 2.38e-18 297-322
1002	IPB000822	Zinc finger, C2H2 type	14.67 2.50e-19 325-350
1002	IPB000822	Zinc finger, C2H2 type	14.67 7.23e-18 185-210
1002	IPB000822	Zinc finger, C2H2 type	14.67 7.23e-18 241-266
1002	IPB000822	Zinc finger, C2H2 type	14.67 7.75e-20 269-294
1002	IPB001275	DM DNA binding domain	19.17 1.85e-10 201-240
1002	IPB001275	DM DNA binding domain	19.17 4.65e-10 313-352
1002	IPB001275	DM DNA binding domain	19.17 5.50e-10 257-296
1002	IPB001275	DM DNA binding domain	19.17 6.24e-12 285-324

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1002	IPB001275	DM DNA binding domain	19.17 8.66e-10 229-268
1002	PR00048A	C2H2-type zinc finger signature I	9.94 1.00e-09 210-223
1002	PR00048A	C2H2-type zinc finger signature I	9.94 1.38e-09 182-195
1002	PR00048A	C2H2-type zinc finger signature I	9.94 1.41e-10 350-363
1002	PR00048A	C2H2-type zinc finger signature I	9.94 1.53e-12 238-251
1002	PR00048A	C2H2-type zinc finger signature I	9.94 1.95e-11 294-307
1002	PR00048A	C2H2-type zinc finger signature I	9.94 2.50e-09 322-335
1002	PR00048A	C2H2-type zinc finger signature I	9.94 6.79e-13 266-279
1002	PR00048B	C2H2-type zinc finger signature II	5.52 2.00e-09 198-207
1002	PR00048B	C2H2-type zinc finger signature II	5.52 5.50e-10 310-319
1002	PR00048B	C2H2-type zinc finger signature II	5.52 9.00e-09 338-347
1002	PR00048B	C2H2-type zinc finger signature II	5.52 9.36e-10 282-291
1003	IPB000822	Zinc finger, C2H2 type	14.67 1.00e-17 467-492
1003	IPB000822	Zinc finger, C2H2 type	14.67 2.50e-20 523-548
1003	IPB000822	Zinc finger, C2H2 type	14.67 2.80e-16 262-287
1003	IPB000822	Zinc finger, C2H2 type	14.67 2.93e-17 439-464
1003	IPB000822	Zinc finger, C2H2 type	14.67 4.27e-21 383-408
1003	IPB000822	Zinc finger, C2H2 type	14.67 4.60e-16 663-688
1003	IPB000822	Zinc finger, C2H2 type	14.67 4.94e-15 635-660
1003	IPB000822	Zinc finger, C2H2 type	14.67 5.09e-21 411-436
1003	IPB000822	Zinc finger, C2H2 type	14.67 5.91e-21 495-520
1003	IPB000822	Zinc finger, C2H2 type	14.67 6.25e-19 327-352
1003	IPB000822	Zinc finger, C2H2 type	14.67 6.25e-20 579-604
1003	IPB000822	Zinc finger, C2H2 type	14.67 6.54e-18 355-380
1003	IPB000822	Zinc finger, C2H2 type	14.67 6.79e-17 299-324
1003	IPB000822	Zinc finger, C2H2 type	14.67 8.20e-22 607-632
1003	IPB000822	Zinc finger, C2H2 type	14.67 8.71e-17 551-576
1003	IPB001275	DM DNA binding domain	19.17 3.69e-12 371-410
1003	IPB001275	DM DNA binding domain	19.17 4.21e-11 399-438
1003	IPB001275	DM DNA binding domain	19.17 4.21e-11 483-522
1003	IPB001275	DM DNA binding domain	19.17 4.89e-10 539-578
1003	IPB001275	DM DNA binding domain	19.17 5.57e-13 595-634
1003	IPB001275	DM DNA binding domain	19.17 6.35e-10 455-494
1003	IPB001275	DM DNA binding domain	19.17 7.56e-11 511-550
1003	IPB001275	DM DNA binding domain	19.17 8.42e-10 343-382
1003	IPB001275	DM DNA binding domain	19.17 9.03e-10 651-690
1003	IPB001275	DM DNA binding domain	19.17 9.09e-09 287-326
1003	IPB001275	DM DNA binding domain	19.17 9.14e-13 567-606
1003	IPB001275	DM DNA binding domain	19.17 9.64e-10 315-354
1003	PR00048A	C2H2-type zinc finger signature I	9.94 1.00e-08 548-561
1003	PR00048A	C2H2-type zinc finger signature I	9.94 1.82e-10 259-272
1003	PR00048A	C2H2-type zinc finger signature I	9.94 2.06e-12 464-477
1003	PR00048A	C2H2-type zinc finger signature I	9.94 2.93e-13 604-617
1003	PR00048A	C2H2-type zinc finger signature I	9.94 3.25e-09 324-337
1003	PR00048A	C2H2-type zinc finger signature I	9.94 4.27e-10 520-533
1003	PR00048A	C2H2-type zinc finger signature I	9.94 4.86e-13 380-393
1003	PR00048A	C2H2-type zinc finger signature I	9.94 5.15e-14 576-589
1003	PR00048A	C2H2-type zinc finger signature I	9.94 6.54e-14 408-421
1003	PR00048A	C2H2-type zinc finger signature I	9.94 6.73e-10 436-449
1003	PR00048A	C2H2-type zinc finger signature I	9.94 7.23e-14 492-505
1003	PR00048A	C2H2-type zinc finger signature I	9.94 7.35e-12 352-365
1003	PR00048A	C2H2-type zinc finger signature I	9.94 8.88e-09 632-645
1003	PR00048A	C2H2-type zinc finger signature I	9.94 9.53e-11 660-673

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SEQ ID NO:	Database entry ID	Description	Results*
1003	PR00048B	C2H2-type zinc finger signature II	5.52 2.50e-09 676-685
1003	PR00048B	C2H2-type zinc finger signature II	5.52 3.57e-10 508-517
1003	PR00048B	C2H2-type zinc finger signature II	5.52 3.57e-10 536-545
1003	PR00048B	C2H2-type zinc finger signature II	5.52 3.57e-10 620-629
1003	PR00048B	C2H2-type zinc finger signature II	5.52 4.00e-09 592-601
1003	PR00048B	C2H2-type zinc finger signature II	5.52 4.86e-10 312-321
1003	PR00048B	C2H2-type zinc finger signature II	5.52 4.86e-10 396-405
1003	PR00048B	C2H2-type zinc finger signature II	5.52 6.14e-10 340-349
1003	PR00048B	C2H2-type zinc finger signature II	5.52 7.75e-11 424-433
1003	PR00048B	C2H2-type zinc finger signature II	5.52 8.00e-09 368-377
1003	PR00048B	C2H2-type zinc finger signature II	5.52 9.00e-09 564-573
1007	IPB001781	LIM domain	11.42 1.00e-09 536-546
1007	IPB001781	LIM domain	11.42 8.11e-12 469-479
1007	IPB001781	LIM domain	11.42 9.59e-11 411-421
1010	IPB000822	Zinc finger, C2H2 type	14.67 2.88e-09 156-181
1011	PR00456F	Ribosomal protein P2 signature VI	5.70 6.76e-12 76-87
1016	IPB002087A	Anti-proliferative protein	15.38 5.68e-13 14-28
1016	IPB002087B	Anti-proliferative protein	19.44 6.88e-20 122-155
1016	IPB002087C	Anti-proliferative protein	13.79 1.00e-23 180-200
1016	PR00310A	Anti-proliferative protein BTG1 family signature I	10.74 2.45e-28 16-40
1016	PR00310B	Anti-proliferative protein BTG1 family signature II	10.25 6.14e-24 123-152
1016	PR00310C	Anti-proliferative protein BTG1 family signature III	12.94 8.41e-36 153-182
1016	PR00310D	Anti-proliferative protein BTG1 family signature IV	9.99 4.71e-38 183-212
1016	PR00310E	Anti-proliferative protein BTG1 family signature V	14.23 2.06e-24 229-248
1017	IPB000306	FYVE Zn-finger, rabphilin/VPS27/FAB1 type	8.96 9.74e-09 491-503
1017	IPB000822	Zinc finger, C2H2 type	14.67 1.64e-17 411-436
1017	IPB000822	Zinc finger, C2H2 type	14.67 1.64e-17 523-548
1017	IPB000822	Zinc finger, C2H2 type	14.67 3.00e-24 383-408
1017	IPB000822	Zinc finger, C2H2 type	14.67 3.25e-20 355-380
1017	IPB000822	Zinc finger, C2H2 type	14.67 4.27e-21 467-492
1017	IPB000822	Zinc finger, C2H2 type	14.67 4.86e-11 215-240
1017	IPB000822	Zinc finger, C2H2 type	14.67 4.94e-14 271-296
1017	IPB000822	Zinc finger, C2H2 type	14.67 5.50e-09 121-146
1017	IPB000822	Zinc finger, C2H2 type	14.67 6.79e-17 439-464
1017	IPB000822	Zinc finger, C2H2 type	14.67 8.50e-20 327-352
1017	IPB000822	Zinc finger, C2H2 type	14.67 8.62e-18 495-520
1017	IPB000822	Zinc finger, C2H2 type	14.67 8.71e-10 149-174
1017	IPB001275	DM DNA binding domain	19.17 5.24e-11 343-382
1017	IPB001275	DM DNA binding domain	19.17 5.38e-10 483-522
1017	IPB001275	DM DNA binding domain	19.17 6.35e-09 315-354
1017	IPB001275	DM DNA binding domain	19.17 8.06e-09 427-466
1017	IPB001275	DM DNA binding domain	19.17 8.18e-09 455-494
1017	IPB001275	DM DNA binding domain	19.17 8.78e-10 511-550
1017	IPB001275	DM DNA binding domain	19.17 9.61e-11 371-410
1017	IPB001909	KRAB box	17.37 2.50e-33 44-78
1017	PR00048A	C2H2-type zinc finger signature I	9.94 1.00e-13 408-421
1017	PR00048A	C2H2-type zinc finger signature I	9.94 5.09e-10 324-337
1017	PR00048A	C2H2-type zinc finger signature I	9.94 5.24e-12 436-449

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SEQ ID NO:	Database entry ID	Description	Results*
1017	PR00048A	C2H2-type zinc finger signature I	9.94 6.54e-14 380-393
1017	PR00048A	C2H2-type zinc finger signature I	9.94 6.73e-10 492-505
1017	PR00048A	C2H2-type zinc finger signature I	9.94 6.79e-13 464-477
1017	PR00048A	C2H2-type zinc finger signature I	9.94 7.88e-12 352-365
1017	PR00048A	C2H2-type zinc finger signature I	9.94 8.13e-09 268-281
1017	PR00048A	C2H2-type zinc finger signature I	9.94 9.10e-15 520-533
1017	PR00048B	C2H2-type zinc finger signature II	5.52 2.50e-09 340-349
1017	PR00048B	C2H2-type zinc finger signature II	5.52 3.25e-11 396-405
1017	PR00048B	C2H2-type zinc finger signature II	5.52 3.25e-11 508-517
1017	PR00048B	C2H2-type zinc finger signature II	5.52 7.00e-11 368-377
1017	PR00048B	C2H2-type zinc finger signature II	5.52 9.36e-10 480-489
1020	IPB001781	LIM domain	11.42 1.69e-10 160-170
1020	IPB001781	LIM domain	11.42 1.95e-12 219-229
1020	IPB001781	LIM domain	11.42 5.26e-12 99-109
1022	PR01217G	Proline rich extensin signature VII	4.02 6.61e-09 130-155
1024	IPB000822	Zinc finger, C2H2 type	14.67 1.00e-16 410-435
1024	IPB000822	Zinc finger, C2H2 type	14.67 3.25e-19 326-351
1024	IPB000822	Zinc finger, C2H2 type	14.67 3.25e-20 214-239
1024	IPB000822	Zinc finger, C2H2 type	14.67 3.77e-18 242-267
1024	IPB000822	Zinc finger, C2H2 type	14.67 4.00e-19 382-407
1024	IPB000822	Zinc finger, C2H2 type	14.67 4.75e-20 270-295
1024	IPB000822	Zinc finger, C2H2 type	14.67 4.94e-14 298-323
1024	IPB000822	Zinc finger, C2H2 type	14.67 5.50e-09 158-183
1024	IPB000822	Zinc finger, C2H2 type	14.67 6.00e-13 186-211
1024	IPB000822	Zinc finger, C2H2 type	14.67 8.07e-17 354-379
1024	IPB001275	DM DNA binding domain	19.17 1.68e-09 398-437
1024	IPB001275	DM DNA binding domain	19.17 3.07e-10 314-353
1024	IPB001275	DM DNA binding domain	19.17 5.37e-11 370-409
1024	IPB001275	DM DNA binding domain	19.17 5.74e-10 258-297
1024	IPB001275	DM DNA binding domain	19.17 6.10e-12 202-241
1024	IPB001275	DM DNA binding domain	19.17 8.12e-12 342-381
1024	IPB001275	DM DNA binding domain	19.17 9.66e-09 230-269
1024	IPB001502E	Endonuclease III	23.53 7.04e-09 252-279
1024	IPB001909	KRAB box	17.37 9.00e-33 17-51
1024	IPB002867C	Cysteine-rich domain (C6HC)	19.46 3.37e-09 323-340
1024	IPB002867C	Cysteine-rich domain (C6HC)	19.46 9.05e-09 267-284
1024	PR00048A	C2H2-type zinc finger signature I	9.94 1.82e-10 211-224
1024	PR00048A	C2H2-type zinc finger signature I	9.94 1.90e-15 351-364
1024	PR00048A	C2H2-type zinc finger signature I	9.94 2.23e-10 379-392
1024	PR00048A	C2H2-type zinc finger signature I	9.94 6.29e-12 323-336
1024	PR00048A	C2H2-type zinc finger signature I	9.94 7.43e-13 267-280
1024	PR00048A	C2H2-type zinc finger signature I	9.94 7.55e-10 295-308
1024	PR00048A	C2H2-type zinc finger signature I	9.94 8.58e-11 407-420
1024	PR00048A	C2H2-type zinc finger signature I	9.94 8.62e-14 239-252
1024	PR00048B	C2H2-type zinc finger signature II	5.52 5.50e-10 227-236
1024	PR00048B	C2H2-type zinc finger signature II	5.52 6.00e-09 423-432
1024	PR00048B	C2H2-type zinc finger signature II	5.52 8.07e-10 283-292
1024	PR00048B	C2H2-type zinc finger signature II	5.52 8.07e-10 339-348
1024	PR00048B	C2H2-type zinc finger signature II	5.52 8.07e-10 395-404
1025	PR00966H	Potyvirus nuclear inclusion A cysteine protease (C4) signature VIII	13.43 9.45e-09 215-234
1026	IPB000315A	B-box zinc finger superfamily	24.51 4.67e-12 19-42
1026	IPB001293A	TRAF-type zinc finger	26.83 8.34e-10 10-54

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SEQ ID NO:	Database entry ID	Description	Results*
1026	IPB003649A	B-Box C-terminal domain	13.56 7.92e-12 26-39
1026	PR00194D	Tropomyosin signature IV	9.54 7.21e-10 150-173
1026	PR01511F	Kv1.4 voltage-gated K ⁺ channel signature VI	5.19 4.54e-09 141-155
1029	IPB000006	Vertebrate metallothionein, family 1	13.41 6.13e-10 91-136
1029	IPB000006	Vertebrate metallothionein, family 1	13.41 6.23e-09 71-116
1029	IPB000118A	Granulin	8.25 8.84e-09 141-163
1029	IPB000359B	Cystine-knot domain	19.26 9.44e-09 181-199
1029	IPB000726B	Glycoside hydrolase family 19	5.39 2.54e-09 66-76
1029	IPB000967E	Zinc finger NF-X1 type	21.88 6.54e-09 105-145
1029	IPB000967E	Zinc finger NF-X1 type	21.88 7.83e-10 183-223
1029	IPB000967E	Zinc finger NF-X1 type	21.88 9.04e-09 136-176
1029	IPB001169K	Integrin beta, C-terminus	27.45 6.96e-09 107-149
1029	IPB001169K	Integrin beta, C-terminus	27.45 7.93e-09 56-98
1029	IPB001762A	Disintegrin	23.93 6.47e-09 185-225
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.84e-10 102-135
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.08e-13 164-197
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.25e-10 66-99
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.25e-10 92-125
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.46e-11 112-145
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.68e-11 169-202
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.89e-12 122-155
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.00e-14 159-192
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.39e-09 174-207
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.64e-11 206-239
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.19e-10 107-140
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.65e-09 91-124
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.04e-14 76-109
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.19e-13 81-114
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.71e-09 8-41
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.88e-15 117-150
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.00e-09 221-254
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.10e-09 67-100
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.48e-09 222-255
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.16e-09 216-249
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.33e-12 196-229
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.38e-13 71-104
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.84e-09 197-230
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.03e-09 86-119
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.28e-10 154-187
1029	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.32e-09 57-90
1029	IPB002494B	Keratin, high sulfur B2 protein	10.58 1.13e-09 70-84
1029	IPB002494B	Keratin, high sulfur B2 protein	10.58 2.01e-09 136-150
1029	IPB002494B	Keratin, high sulfur B2 protein	10.58 3.15e-10 22-36
1029	IPB002494B	Keratin, high sulfur B2 protein	10.58 5.94e-09 215-229
1029	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.20e-09 105-119
1029	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.58e-09 163-177
1029	IPB002494B	Keratin, high sulfur B2 protein	10.58 7.85e-10 210-224
1029	IPB002494B	Keratin, high sulfur B2 protein	10.58 8.23e-09 234-248
1029	IPB002494B	Keratin, high sulfur B2 protein	10.58 8.66e-10 95-109
1029	IPB002494B	Keratin, high sulfur B2 protein	10.58 9.62e-09 121-135
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.10e-14 31-74
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.11e-17 69-112

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SEQ ID NO:	Database entry ID	Description	Results*
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.27e-11 27-70
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.27e-11 59-102
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.39e-13 199-242
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.64e-11 114-157
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.72e-15 104-147
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.79e-10 204-247
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.22e-12 100-143
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.35e-09 135-178
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.43e-09 177-220
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.80e-18 115-158
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.16e-19 162-205
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.20e-14 120-163
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.45e-13 94-137
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.79e-15 167-210
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.94e-09 85-128
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.03e-13 26-69
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.42e-13 64-107
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.72e-13 95-138
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.83e-15 84-127
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.00e-14 172-215
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.37e-09 183-226
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.38e-20 209-252
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.50e-12 219-262
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.71e-09 147-190
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.79e-09 70-113
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.09e-13 99-142
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.33e-10 90-133
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.42e-10 32-75
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.14e-09 142-185
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.16e-13 130-173
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.38e-19 157-200
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.39e-20 79-122
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.15e-09 16-59
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.15e-09 80-123
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.29e-19 110-153
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.36e-11 109-152
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.41e-12 125-168
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.45e-15 89-132
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.57e-09 189-232
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.86e-15 11-54
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.92e-13 152-195
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.13e-17 21-64
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.16e-21 74-117
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.27e-11 6-49
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.71e-13 36-79
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.75e-09 41-84
1029	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.80e-14 105-148
1029	IPB002919A	Trypsin Inhibitor-like cysteine rich domain	15.56 5.71e-09 24-36
1031	IPB002130A	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	13.87 2.17e-15 18-39
1031	IPB002130B	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	21.20 5.85e-39 48-86
1031	IPB002130C	Cyclophilin-type peptidyl-prolyl cis-trans	16.92 1.00e-40 98-135

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SEQ ID NO:	Database entry ID	Description	Results*
		isomerase	
1031	PR00153A	Cyclophilin peptidyl-prolyl cis-trans isomerase signature I	14.60 2.71e-10 24-39
1031	PR00153B	Cyclophilin peptidyl-prolyl cis-trans isomerase signature II	12.94 6.29e-17 53-65
1031	PR00153C	Cyclophilin peptidyl-prolyl cis-trans isomerase signature III	10.79 2.64e-20 96-111
1031	PR00153D	Cyclophilin peptidyl-prolyl cis-trans isomerase signature IV	10.73 1.47e-15 111-123
1031	PR00153E	Cyclophilin peptidyl-prolyl cis-trans isomerase signature V	8.39 1.43e-15 124-139
1032	PR00010C	Type II EGF-like signature III	6.98 5.17e-09 45-55
1035	IPB000822	Zinc finger, C2H2 type	14.67 1.69e-18 274-299
1035	IPB000822	Zinc finger, C2H2 type	14.67 2.29e-17 102-127
1035	IPB000822	Zinc finger, C2H2 type	14.67 2.29e-17 302-327
1035	IPB000822	Zinc finger, C2H2 type	14.67 3.77e-18 190-215
1035	IPB000822	Zinc finger, C2H2 type	14.67 3.81e-15 414-439
1035	IPB000822	Zinc finger, C2H2 type	14.67 4.75e-19 218-243
1035	IPB000822	Zinc finger, C2H2 type	14.67 4.75e-19 442-467
1035	IPB000822	Zinc finger, C2H2 type	14.67 5.50e-15 162-187
1035	IPB000822	Zinc finger, C2H2 type	14.67 6.25e-19 386-411
1035	IPB000822	Zinc finger, C2H2 type	14.67 6.25e-20 358-383
1035	IPB000822	Zinc finger, C2H2 type	14.67 6.50e-13 246-271
1035	IPB000822	Zinc finger, C2H2 type	14.67 6.79e-17 330-355
1035	IPB000822	Zinc finger, C2H2 type	14.67 7.00e-19 470-495
1035	IPB000822	Zinc finger, C2H2 type	14.67 7.23e-18 498-523
1035	IPB000822	Zinc finger, C2H2 type	14.67 8.07e-17 526-551
1035	IPB000822	Zinc finger, C2H2 type	14.67 8.50e-19 134-159
1035	IPB001275	DM DNA binding domain	19.17 1.34e-09 206-245
1035	IPB001275	DM DNA binding domain	19.17 2.70e-10 178-217
1035	IPB001275	DM DNA binding domain	19.17 3.55e-10 374-413
1035	IPB001275	DM DNA binding domain	19.17 4.08e-09 346-385
1035	IPB001275	DM DNA binding domain	19.17 5.86e-10 458-497
1035	IPB001275	DM DNA binding domain	19.17 8.78e-10 318-357
1035	IPB001275	DM DNA binding domain	19.17 9.15e-10 290-329
1035	IPB001275	DM DNA binding domain	19.17 9.88e-10 486-525
1035	IPB001909	KRAB box	17.37 3.86e-28 6-40
1035	PR00048A	C2H2-type zinc finger signature I	9.94 1.41e-10 187-200
1035	PR00048A	C2H2-type zinc finger signature I	9.94 2.29e-13 299-312
1035	PR00048A	C2H2-type zinc finger signature I	9.94 2.42e-11 131-144
1035	PR00048A	C2H2-type zinc finger signature I	9.94 2.64e-10 383-396
1035	PR00048A	C2H2-type zinc finger signature I	9.94 3.45e-10 411-424
1035	PR00048A	C2H2-type zinc finger signature I	9.94 4.18e-12 495-508
1035	PR00048A	C2H2-type zinc finger signature I	9.94 4.21e-13 523-536
1035	PR00048A	C2H2-type zinc finger signature I	9.94 5.09e-10 551-564
1035	PR00048A	C2H2-type zinc finger signature I	9.94 6.14e-13 327-340
1035	PR00048A	C2H2-type zinc finger signature I	9.94 6.14e-13 99-112
1035	PR00048A	C2H2-type zinc finger signature I	9.94 6.54e-14 215-228
1035	PR00048A	C2H2-type zinc finger signature I	9.94 6.54e-14 467-480
1035	PR00048A	C2H2-type zinc finger signature I	9.94 6.82e-12 243-256
1035	PR00048A	C2H2-type zinc finger signature I	9.94 7.92e-14 355-368
1035	PR00048A	C2H2-type zinc finger signature I	9.94 8.58e-11 159-172
1035	PR00048A	C2H2-type zinc finger signature I	9.94 9.05e-11 439-452
1035	PR00048A	C2H2-type zinc finger signature I	9.94 9.36e-13 271-284

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SEQ ID NO:	Database entry ID	Description	Results*
1035	PR00048B	C2H2-type zinc finger signature II	5.52 1.00e-08 483-492
1035	PR00048B	C2H2-type zinc finger signature II	5.52 5.00e-12 115-124
1035	PR00048B	C2H2-type zinc finger signature II	5.52 5.50e-10 203-212
1035	PR00048B	C2H2-type zinc finger signature II	5.52 5.50e-10 287-296
1035	PR00048B	C2H2-type zinc finger signature II	5.52 5.50e-11 455-464
1035	PR00048B	C2H2-type zinc finger signature II	5.52 7.50e-09 371-380
1035	PR00048B	C2H2-type zinc finger signature II	5.52 8.00e-09 147-156
1035	PR00048B	C2H2-type zinc finger signature II	5.52 8.50e-09 399-408
1038	IPB001902A	Sulfate transporter	10.29 9.57e-10 310-319
1038	IPB001902B	Sulfate transporter	21.91 3.43e-31 340-390
1038	IPB001902C	Sulfate transporter	23.62 6.44e-25 429-480
1038	IPB002645B	STAS domain	13.24 1.43e-11 179-193
1038	IPB002645B	STAS domain	13.24 1.43e-11 622-636
1039	IPB000626	Ubiquitin domain	21.25 7.65e-09 56-110
1041	IPB000729A	PMP-22/EMP/MP20 family	19.70 9.05e-09 47-68
1042	IPB003530A	Long hematopoietin receptor, soluble alpha chains	23.64 3.01e-09 362-416
1042	PR01474F	Vascular cell adhesion molecule-1 (VCAM-1) signature VI	14.81 9.48e-09 389-402
1043	IPB001526A	Ly-6/u-PAR domain	13.24 3.65e-13 73-88
1043	IPB001526C	Ly-6/u-PAR domain	13.04 6.82e-13 142-157
1043	IPB003605A	GS motif preceding kinase domain in TGF beta receptor	13.79 3.93e-09 149-160
1047	IPB000353B	Class II histocompatibility antigen, beta chain, beta-1 domain	19.16 5.99e-10 203-252
1047	IPB001039A	Major histocompatibility complex protein, Class I	17.17 1.00e-40 15-68
1047	IPB001039B	Major histocompatibility complex protein, Class I	27.55 1.00e-40 96-147
1047	IPB001039C	Major histocompatibility complex protein, Class I	19.82 1.00e-40 177-230
1047	IPB001039D	Major histocompatibility complex protein, Class I	16.49 4.43e-38 255-309
1047	IPB003006A	Immunoglobulin and major histocompatibility complex domain	17.51 3.84e-15 224-246
1047	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 6.25e-25 261-298
1047	IPB003363E	Glycoprotein GG/GX	13.35 2.94e-11 308-340
1051	IPB000729D	PMP-22/EMP/MP20 family	18.96 7.30e-10 173-200
1052	IPB001526C	Ly-6/u-PAR domain	13.04 1.77e-09 46-61
1054	PR00258B	Speract receptor signature II	7.94 9.50e-16 738-749
1054	PR00258C	Speract receptor signature III	9.05 2.32e-10 753-763
1054	PR00258D	Speract receptor signature IV	14.29 6.63e-09 785-799
1054	PR00258E	Speract receptor signature V	14.06 8.45e-14 808-820
1055	IPB001429A	ATP P2X receptor	17.17 1.00e-38 12-50
1055	IPB001429B	ATP P2X receptor	5.49 2.71e-12 62-71
1055	IPB001429C	ATP P2X receptor	19.96 5.68e-31 88-118
1055	IPB001429D	ATP P2X receptor	20.63 2.38e-19 143-164
1055	IPB001429E	ATP P2X receptor	15.32 1.43e-30 178-205
1055	IPB001429F	ATP P2X receptor	20.01 5.88e-30 248-277
1055	IPB001429G	ATP P2X receptor	9.93 2.64e-14 291-300
1055	IPB001429H	ATP P2X receptor	12.67 7.00e-34 309-335
1055	IPB001675B	Glycosyltransferase family 29	15.84 9.26e-09 339-361
1055	PR01307A	P2X purinoceptor family signature I	10.92 2.80e-12 82-90

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SEQ ID NO:	Database entry ID	Description	Results*
1055	PR01307B	P2X purinoceptor family signature II	10.30 1.00e-15 157-168
1055	PR01307C	P2X purinoceptor family signature III	10.17 3.77e-15 243-255
1055	PR01307D	P2X purinoceptor family signature IV	10.26 1.56e-15 290-300
1055	PR01307E	P2X purinoceptor family signature V	15.20 2.29e-19 310-324
1055	PR01311A	P2X4 purinoceptor signature I	7.73 8.32e-10 1-8
1055	PR01311C	P2X4 purinoceptor signature III	9.00 1.90e-12 30-38
1055	PR01311D	P2X4 purinoceptor signature IV	12.87 1.12e-10 49-55
1055	PR01311E	P2X4 purinoceptor signature V	6.43 1.00e-09 139-146
1055	PR01311F	P2X4 purinoceptor signature VI	9.15 1.15e-10 208-216
1055	PR01311G	P2X4 purinoceptor signature VII	11.74 8.00e-14 280-290
1055	PR01311H	P2X4 purinoceptor signature VIII	12.12 1.00e-12 303-312
1055	PR01311I	P2X4 purinoceptor signature IX	5.25 1.00e-11 359-366
1059	PR00854A	Prostaglandin D receptor signature I	15.24 9.08e-18 6-20
1059	PR00854B	Prostaglandin D receptor signature II	7.30 8.15e-21 41-58
1059	PR00854C	Prostaglandin D receptor signature III	12.92 1.64e-12 93-104
1059	PR00854D	Prostaglandin D receptor signature IV	9.41 2.50e-18 185-200
1059	PR00854E	Prostaglandin D receptor signature V	10.50 4.65e-26 236-259
1059	PR00854F	Prostaglandin D receptor signature VI	12.83 9.68e-11 321-332
1059	PR00854G	Prostaglandin D receptor signature VII	10.66 1.78e-18 341-357
1059	PR00854H	Prostaglandin D receptor signature VIII	14.71 6.20e-17 369-389
1059	PR00856E	Prostacyclin (prostanoid IP) receptor signature V	9.82 1.72e-09 178-194
1060	IPB001898A	Sodium:sulfate symporter family	13.06 5.30e-21 49-72
1060	IPB001898B	Sodium:sulfate symporter family	13.18 8.41e-22 88-114
1060	IPB001898C	Sodium:sulfate symporter family	9.97 1.00e-23 132-151
1060	IPB001898D	Sodium:sulfate symporter family	12.13 1.00e-21 208-232
1060	IPB001898E	Sodium:sulfate symporter family	13.97 6.76e-21 248-272
1060	IPB001898F	Sodium:sulfate symporter family	18.66 6.04e-20 309-335
1060	IPB001898G	Sodium:sulfate symporter family	16.36 8.36e-24 405-434
1060	IPB001898H	Sodium:sulfate symporter family	21.26 1.00e-40 486-534
1063	IPB001039A	Major histocompatibility complex protein, Class I	17.17 8.89e-11 19-72
1064	IPB001171A	Ergosterol biosynthesis ERG4/ERG24 enzymes	11.99 1.55e-10 11-24
1064	IPB001171B	Ergosterol biosynthesis ERG4/ERG24 enzymes	14.81 6.88e-15 166-178
1064	IPB001171C	Ergosterol biosynthesis ERG4/ERG24 enzymes	26.44 4.75e-33 181-217
1064	IPB001171D	Ergosterol biosynthesis ERG4/ERG24 enzymes	20.69 1.00e-40 241-282
1064	IPB001171G	Ergosterol biosynthesis ERG4/ERG24 enzymes	25.35 1.00e-40 298-350
1065	IPB003388E	Reticulon	14.24 6.29e-09 930-972
1066	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 2.04e-09 264-301
1067	IPB000276A	Rhodopsin-like GPCR superfamily	11.56 5.20e-12 105-116
1067	PR00237C	Rhodopsin-like GPCR superfamily signature III	14.77 6.73e-11 91-113
1067	PR00237E	Rhodopsin-like GPCR superfamily signature V	13.03 4.77e-10 175-198
1067	PR00245A	Olfactory receptor signature I	10.98 3.65e-09 79-90
1067	PR00245B	Olfactory receptor signature II	13.73 4.60e-09 116-128
1067	PR00245D	Olfactory receptor signature IV	9.34 1.53e-13 212-221
1067	PR00245E	Olfactory receptor signature V	8.96 3.30e-10 259-270

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SEQ ID NO:	Database entry ID	Description	Results*
1067	PR00534A	Melanocortin receptor family signature I	12.77 8.43e-09 38-50
1069	IPB000095E	PAK-box /P21-Rho-binding	17.62 3.52e-11 410-455
1069	IPB000961C	Protein kinase C-terminal domain	15.48 9.39e-14 409-443
1069	IPB001245A	Tyrosine kinase catalytic domain	22.45 6.54e-15 402-442
1069	IPB001245B	Tyrosine kinase catalytic domain	21.68 6.18e-09 467-505
1069	IPB003527C	MAP kinase	14.70 7.37e-10 394-442
1069	IPB003605A	GS motif preceding kinase domain in TGF beta receptor	13.79 2.00e-13 92-103
1069	IPB003605C	GS motif preceding kinase domain in TGF beta receptor	14.92 1.00e-40 302-349
1069	IPB003605D	GS motif preceding kinase domain in TGF beta receptor	12.41 1.00e-40 398-439
1069	IPB003605E	GS motif preceding kinase domain in TGF beta receptor	21.14 1.64e-40 441-480
1069	IPB003605F	GS motif preceding kinase domain in TGF beta receptor	23.21 1.00e-40 504-557
1069	PR00109E	Tyrosine kinase catalytic domain signature V	12.99 5.58e-09 549-571
1070	IPB000729C	PMP-22/EMP/MP20 family	37.83 1.71e-09 80-132
1070	IPB000729D	PMP-22/EMP/MP20 family	18.96 9.33e-10 156-183
1071	IPB000353B	Class II histocompatibility antigen, beta chain, beta-1 domain	19.16 7.52e-14 201-250
1071	IPB001039A	Major histocompatibility complex protein, Class I	17.17 2.80e-26 14-67
1071	IPB001039B	Major histocompatibility complex protein, Class I	27.55 5.50e-23 90-141
1071	IPB001039C	Major histocompatibility complex protein, Class I	19.82 7.75e-16 176-229
1071	IPB001039C	Major histocompatibility complex protein, Class I	19.82 7.94e-23 175-228
1071	IPB001039D	Major histocompatibility complex protein, Class I	16.49 7.43e-29 254-308
1071	IPB003006A	Immunoglobulin and major histocompatibility complex domain	17.51 6.82e-17 222-244
1071	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 6.40e-19 260-297
1072	IPB002146	ATP synthase B/B' CF(0)	21.39 6.94e-09 188-226
1072	PR00308B	Type I antifreeze protein signature II	3.38 8.99e-09 3-14
1072	PR00308C	Type I antifreeze protein signature III	2.79 6.92e-09 3-12
1072	PR00308C	Type I antifreeze protein signature III	2.79 9.59e-10 4-13
1072	PR00308C	Type I antifreeze protein signature III	2.79 9.59e-10 5-14
1072	PR00698E	C.elegans Srg family integral membrane protein signature V	14.65 2.76e-09 111-136
1072	PR01511D	Kv1.4 voltage-gated K+ channel signature IV	3.91 2.29e-09 4-14
1072	PR01511D	Kv1.4 voltage-gated K+ channel signature IV	3.91 2.88e-09 5-15
1073	IPB002617C	Vesicular monoamine transporter	16.23 5.03e-10 198-250
1073	PR01035E	Tetracycline resistance protein signature V	10.87 1.00e-08 208-230
1073	PR01035F	Tetracycline resistance protein signature VI	12.88 1.00e-08 499-519
1074	IPB002617C	Vesicular monoamine transporter	16.23 5.03e-10 286-338
1074	PR01035E	Tetracycline resistance protein signature V	10.87 1.00e-08 296-318
1074	PR01035F	Tetracycline resistance protein signature VI	12.88 1.00e-08 587-607
1075	IPB000906A	ZU5 domain	22.49 3.72e-09 58-100

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SEQ ID NO:	Database entry ID	Description	Results*
1075	IPB000906G	ZU5 domain	25.85 7.95e-10 164-212
1075	PR00806C	Vinculin signature III	10.57 8.56e-09 350-367
1076	PR00237C	Rhodopsin-like GPCR superfamily signature III	14.77 3.25e-09 188-210
1076	PR00237E	Rhodopsin-like GPCR superfamily signature V	13.03 4.86e-09 276-299
1076	PR00237F	Rhodopsin-like GPCR superfamily signature VI	14.34 1.25e-10 322-346
1077	IPB003662A	General substrate transporters	18.97 2.89e-09 139-171
1079	IPB000101A	Gamma-glutamyltranspeptidase	29.14 3.45e-14 352-391
1079	PR01210A	Gamma-glutamyltranspeptidase signature I	17.15 1.50e-13 130-155
1080	IPB000684L	Eukaryotic RNA polymerase II heptapeptide repeat	3.49 8.35e-09 1357-1399
1080	IPB001237C	43 Kd postsynaptic protein	5.44 4.63e-11 28-80
1080	IPB001359H	Synapsin	22.58 8.69e-09 1371-1421
1081	IPB002688A	Sterol/diacylglycerol O-acyltransferase	19.24 8.65e-20 259-281
1081	IPB002688B	Sterol/diacylglycerol O-acyltransferase	22.16 2.50e-25 308-347
1081	IPB002688C	Sterol/diacylglycerol O-acyltransferase	22.98 3.13e-20 321-368
1081	IPB002688D	Sterol/diacylglycerol O-acyltransferase	24.36 3.57e-33 380-415
1081	IPB002688E	Sterol/diacylglycerol O-acyltransferase	13.67 2.50e-18 433-453
1082	PR01547A	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature I	10.65 6.40e-24 53-74
1082	PR01547B	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature II	17.77 2.38e-19 97-116
1082	PR01547C	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature III	9.50 5.94e-23 118-139
1082	PR01547D	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature IV	12.09 5.50e-29 144-169
1082	PR01547E	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature V	10.42 1.95e-26 171-195
1082	PR01547F	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature VI	11.64 5.95e-25 258-278
1082	PR01547G	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature VII	7.91 1.00e-36 298-325
1082	PR01547H	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature VIII	9.70 1.00e-30 333-357
1082	PR01547I	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature IX	15.37 7.94e-28 408-438
1082	PR01547J	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature X	14.06 3.15e-23 439-460
1082	PR01547K	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature XI	13.61 7.87e-23 462-481
1082	PR01547L	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature XII	10.35 6.29e-19 486-502
1082	PR01547M	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature XIII	10.06 3.44e-12 1178-1196
1083	IPB000095E	PAK-box /P21-Rho-binding	17.62 3.15e-12 367-412
1083	IPB000961C	Protein kinase C-terminal domain	15.48 4.66e-14 366-400
1083	IPB001245A	Tyrosine kinase catalytic domain	22.45 5.50e-14 359-399
1083	IPB001245B	Tyrosine kinase catalytic domain	21.68 6.18e-09 424-462
1083	IPB001526C	Ly-6/u-PAR domain	13.04 1.00e-08 105-120
1083	IPB003527C	MAP kinase	14.70 8.81e-10 351-399
1083	IPB003605A	GS motif preceding kinase domain in TGF beta receptor	13.79 1.32e-11 112-123

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SEQ ID NO:	Database entry ID	Description	Results*
1083	IPB003605B	GS motif preceding kinase domain in TGF beta receptor	10.56 5.00e-28 229-255
1083	IPB003605C	GS motif preceding kinase domain in TGF beta receptor	14.92 1.00e-40 259-306
1083	IPB003605D	GS motif preceding kinase domain in TGF beta receptor	12.41 1.00e-40 355-396
1083	IPB003605E	GS motif preceding kinase domain in TGF beta receptor	21.14 8.88e-39 398-437
1083	IPB003605F	GS motif preceding kinase domain in TGF beta receptor	23.21 6.81e-40 461-514
1083	PR00109E	Tyrosine kinase catalytic domain signature V	12.99 2.15e-09 535-557
1083	PR00653D	Activin type II receptor signature IV	12.01 6.70e-11 385-406
1084	IPB000095E	PAK-box /P21-Rho-binding	17.62 3.15e-12 429-474
1084	IPB000961C	Protein kinase C-terminal domain	15.48 4.66e-14 428-462
1084	IPB001245A	Tyrosine kinase catalytic domain	22.45 5.50e-14 421-461
1084	IPB001245B	Tyrosine kinase catalytic domain	21.68 6.18e-09 486-524
1084	IPB001526C	Ly-6/u-PAR domain	13.04 1.00e-08 105-120
1084	IPB003527C	MAP kinase	14.70 8.81e-10 413-461
1084	IPB003605A	GS motif preceding kinase domain in TGF beta receptor	13.79 1.32e-11 112-123
1084	IPB003605B	GS motif preceding kinase domain in TGF beta receptor	10.56 5.00e-28 291-317
1084	IPB003605C	GS motif preceding kinase domain in TGF beta receptor	14.92 1.00e-40 321-368
1084	IPB003605D	GS motif preceding kinase domain in TGF beta receptor	12.41 1.00e-40 417-458
1084	IPB003605E	GS motif preceding kinase domain in TGF beta receptor	21.14 8.88e-39 460-499
1084	IPB003605F	GS motif preceding kinase domain in TGF beta receptor	23.21 6.81e-40 523-576
1084	PR00109E	Tyrosine kinase catalytic domain signature V	12.99 2.15e-09 597-619
1084	PR00653D	Activin type II receptor signature IV	12.01 6.70e-11 447-468
1085	PR00541C	Muscarinic M4 receptor signature III	8.06 7.73e-09 486-506
1086	PR00541C	Muscarinic M4 receptor signature III	8.06 7.73e-09 755-775
1087	PR01430A	Protease activated receptor 2 precursor signature I	8.72 8.20e-09 123-134
1088	IPB000322A	Glycoside hydrolase family 31	19.86 8.13e-23 151-176
1088	IPB000322B	Glycoside hydrolase family 31	14.24 9.64e-10 186-201
1088	IPB000322C	Glycoside hydrolase family 31	22.80 3.57e-20 225-250
1088	IPB000322D	Glycoside hydrolase family 31	17.98 6.57e-27 326-352
1088	IPB000322E	Glycoside hydrolase family 31	25.60 9.10e-33 366-407
1090	IPB000135A	High mobility group proteins HMG1 and HMG2	11.69 7.66e-14 707-761
1090	IPB000135B	High mobility group proteins HMG1 and HMG2	13.24 5.68e-21 680-724
1090	PR00886A	High mobility group (HMG1/HMG2) protein signature I	10.57 4.46e-10 710-732
1090	PR00886C	High mobility group (HMG1/HMG2) protein signature III	11.20 6.28e-13 696-714
1090	PR00887A	Structure-specific recognition protein signature I	12.71 1.82e-21 343-359
1090	PR00887B	Structure-specific recognition protein	10.24 1.35e-20 365-381

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SEQ ID NO:	Database entry ID	Description	Results*
		signature II	
1090	PR00887C	Structure-specific recognition protein signature III	13.32 1.47e-21 388-404
1090	PR00887D	Structure-specific recognition protein signature IV	16.42 2.73e-15 453-466
1090	PR00887E	Structure-specific recognition protein signature V	10.75 3.40e-20 480-498
1090	PR00887F	Structure-specific recognition protein signature VI	14.12 6.46e-21 498-515
1090	PR00887G	Structure-specific recognition protein signature VII	13.65 7.00e-18 521-537
1090	PR00887H	Structure-specific recognition protein signature VIII	12.27 3.53e-20 537-555
1091	IPB000215A	Serpins	13.01 4.77e-13 341-364
1091	IPB000215B	Serpins	9.87 9.68e-09 449-461
1091	IPB000215C	Serpins	13.90 7.11e-11 476-490
1091	IPB000215D	Serpins	15.35 3.88e-16 578-604
1091	IPB000215E	Serpins	15.36 6.21e-16 659-683
1092	IPB000126A	Serine proteases, V8 family	11.75 2.88e-10 357-372
1092	IPB000126B	Serine proteases, V8 family	12.50 1.51e-11 471-487
1092	PR00834D	HtrA/DegQ protease family signature IV	11.75 6.23e-09 466-483
1092	PR00839B	V8 serine protease family signature II	11.20 8.12e-10 357-374
1097	IPB000454	Eubacterial and plasma membrane ATP synthase subunit C	27.64 2.50e-28 79-132
1097	PR00124A	ATP synthase C subunit signature I	8.69 4.46e-13 75-94
1097	PR00124B	ATP synthase C subunit signature II	14.47 8.14e-11 96-111
1097	PR00124C	ATP synthase C subunit signature III	12.82 6.63e-17 113-138
1098	IPB000573	Aconitase C-terminal domain	25.70 4.86e-34 947-996
1098	IPB001030A	Aconitase (aconitate hydratase)	37.52 1.17e-13 452-500
1098	IPB001030A	Aconitase (aconitate hydratase)	37.52 5.06e-23 392-440
1098	IPB001030B	Aconitase (aconitate hydratase)	18.77 4.32e-18 665-688
1098	IPB001030C	Aconitase (aconitate hydratase)	18.16 3.65e-12 710-724
1098	PR00415A	Aconitase family signature I	13.25 7.00e-10 323-336
1098	PR00415C	Aconitase family signature III	14.58 2.75e-13 376-389
1098	PR00415D	Aconitase family signature IV	14.53 2.93e-15 390-405
1098	PR00415E	Aconitase family signature V	9.37 1.53e-12 452-465
1098	PR00415F	Aconitase family signature VI	11.36 6.14e-12 466-479
1098	PR00415G	Aconitase family signature VII	14.02 2.35e-14 548-562
1098	PR00415H	Aconitase family signature VIII	13.87 4.79e-12 613-624
1098	PR00415I	Aconitase family signature IX	14.82 8.43e-15 675-688
1099	PR01088H	Na ⁺ /H ⁺ exchanger isoform 6 (NHE6) signature VIII	16.89 1.00e-08 92-109
1100	PR01088H	Na ⁺ /H ⁺ exchanger isoform 6 (NHE6) signature VIII	16.89 1.00e-08 188-205
1101	PR01088H	Na ⁺ /H ⁺ exchanger isoform 6 (NHE6) signature VIII	16.89 1.00e-08 142-159
1102	PR00259D	Transmembrane four family signature IV	14.90 2.43e-09 65-91
1104	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 8.56e-10 124-161
1104	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 9.65e-09 227-264
1106	IPB001983A	Translationally controlled tumor protein	14.49 1.43e-25 1-27
1106	IPB001983B	Translationally controlled tumor protein	15.99 4.43e-20 45-70
1106	IPB001983C	Translationally controlled tumor protein	16.91 1.41e-24 83-109

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SEQ ID NO:	Database entry ID	Description	Results*
1106	IPB001983D	Translationally controlled tumor protein	22.98 4.09e-28 123-163
1107	IPB000117D	Kappa casein	10.18 8.71e-09 513-547
1108	IPB001737A	Ribosomal RNA adenine dimethylase	27.11 1.86e-09 110-155
1109	IPB002048	EF-hand family	7.91 1.00e-09 42-54
1110	IPB000272	ATP1G1/PLM/MAT8 family	14.36 8.64e-23 99-134
1110	IPB003403A	Herpesvirus immediate early protein	21.25 6.59e-09 39-61
1112	PR00261B	Low density lipoprotein (LDL) receptor signature II	15.12 6.29e-09 127-148
1112	PR00261D	Low density lipoprotein (LDL) receptor signature IV	16.87 7.09e-09 127-148
1112	PR00261F	Low density lipoprotein (LDL) receptor signature VI	15.46 3.91e-09 127-148
1112	PR00764B	Complement C9 signature II	12.47 1.36e-11 122-142
1115	IPB000276A	Rhodopsin-like GPCR superfamily	11.56 4.32e-10 216-227
1115	PR00245A	Olfactory receptor signature I	10.98 6.70e-10 190-201
1115	PR00245B	Olfactory receptor signature II	13.73 2.03e-09 227-239
1115	PR00245C	Olfactory receptor signature III	14.65 3.54e-10 274-290
1116	IPB000276A	Rhodopsin-like GPCR superfamily	11.56 8.36e-09 5-16
1116	IPB000276D	Rhodopsin-like GPCR superfamily	9.40 6.19e-09 355-371
1116	PR00245A	Olfactory receptor signature I	10.98 3.16e-11 165-176
1116	PR00245B	Olfactory receptor signature II	13.73 1.77e-09 16-28
1116	PR00245B	Olfactory receptor signature II	13.73 9.07e-10 202-214
1116	PR00245C	Olfactory receptor signature III	14.65 2.96e-15 249-265
1116	PR00245D	Olfactory receptor signature IV	9.34 8.58e-12 309-318
1116	PR00245E	Olfactory receptor signature V	8.96 2.20e-15 356-367
1119	IPB001862A	Membrane attack complex components/perforin/complement C9	12.54 1.92e-10 300-315
1119	IPB001862A	Membrane attack complex components/perforin/complement C9	12.54 1.92e-10 565-580
1119	IPB001862A	Membrane attack complex components/perforin/complement C9	12.54 2.83e-11 1213-1228
1119	IPB001862A	Membrane attack complex components/perforin/complement C9	12.54 3.90e-09 143-158
1119	IPB001862A	Membrane attack complex components/perforin/complement C9	12.54 4.77e-09 448-463
1119	IPB001862A	Membrane attack complex components/perforin/complement C9	12.54 7.83e-11 1336-1351
1119	IPB001862A	Membrane attack complex components/perforin/complement C9	12.54 8.02e-10 1093-1108
1119	IPB001862A	Membrane attack complex components/perforin/complement C9	12.54 8.92e-12 964-979
1119	IPB001928	Endothelin and related toxins	14.31 3.00e-09 949-972
1119	IPB002861B	Reeler domain	10.50 5.95e-11 970-998
1119	IPB002861C	Reeler domain	23.17 1.00e-12 957-1011
1119	IPB002861C	Reeler domain	23.17 3.45e-09 136-190
1120	IPB000079	Nucleosomal binding domain found in HMG14 and HMG17	8.09 1.64e-37 18-48
1120	PR00925A	Nonhistone chromosomal protein HMG17 family signature I	5.67 2.29e-19 18-32
1120	PR00925B	Nonhistone chromosomal protein HMG17 family signature II	3.75 3.18e-16 34-46
1120	PR00925C	Nonhistone chromosomal protein HMG17 family signature III	5.23 7.45e-09 47-57
1120	PR00925D	Nonhistone chromosomal protein HMG17	7.38 2.00e-14 66-76

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SEQ ID NO:	Database entry ID	Description	Results*
		family signature IV	
1121	PR00219C	Synaptobrevin signature III	6.91 1.56e-09 89-108
1124	IPB001304A	C-type lectin domain	17.98 8.88e-19 203-227
1125	IPB002896F	Herpesvirus glycoprotein D	21.08 9.22e-09 374-409
1125	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 5.15e-09 323-360
1126	PR01007I	Flagellar hook-length control protein signature IX	8.84 9.69e-09 467-490
1131	IPB000008D	C2 domain	14.83 3.05e-11 1008-1026
1131	IPB000738A	WHEP-TRS domain	22.67 8.02e-09 1068-1093
1131	PR00360A	C2 domain signature I	15.18 8.36e-09 682-694
1132	IPB001135C	NADH-ubiquinone oxidoreductase 49Kd chain	25.46 9.79e-09 72-122
1133	IPB000276A	Rhodopsin-like GPCR superfamily	11.56 2.20e-12 181-192
1133	IPB000276D	Rhodopsin-like GPCR superfamily	9.40 6.09e-10 344-360
1133	PR00237G	Rhodopsin-like GPCR superfamily signature VII	19.23 7.37e-10 334-360
1133	PR00245A	Olfactory receptor signature I	10.98 8.50e-10 155-166
1133	PR00245B	Olfactory receptor signature II	13.73 8.20e-13 192-204
1133	PR00245C	Olfactory receptor signature III	14.65 4.10e-13 239-255
1133	PR00245D	Olfactory receptor signature IV	9.34 7.63e-12 298-307
1133	PR00245E	Olfactory receptor signature V	8.96 4.77e-12 345-356
1134	IPB000425A	MIP family	9.37 7.33e-11 92-107
1134	IPB000425B	MIP family	22.94 1.75e-31 123-175
1134	IPB000425C	MIP family	10.67 7.28e-10 240-254
1134	IPB000425D	MIP family	8.10 9.67e-15 307-325
1134	PR00783A	Major intrinsic protein family signature I	11.82 5.50e-14 88-107
1134	PR00783B	Major intrinsic protein family signature II	15.34 1.67e-19 127-151
1134	PR00783C	Major intrinsic protein family signature III	13.32 2.76e-10 164-183
1134	PR00783E	Major intrinsic protein family signature V	16.25 8.11e-09 128-150
1134	PR00783E	Major intrinsic protein family signature V	16.25 8.13e-11 226-248
1134	PR00783F	Major intrinsic protein family signature VI	12.30 1.53e-14 308-328
1136	IPB002897A	Monocarboxylate transporter	16.12 4.90e-23 18-47
1136	IPB002897B	Monocarboxylate transporter	24.20 4.30e-32 72-126
1136	IPB002897C	Monocarboxylate transporter	13.63 4.46e-13 143-168
1136	IPB002897C	Monocarboxylate transporter	13.63 7.38e-12 177-202
1136	IPB002897D	Monocarboxylate transporter	30.44 5.85e-27 296-348
1136	IPB002897E	Monocarboxylate transporter	32.06 9.59e-24 407-458
1137	IPB000454	Eubacterial and plasma membrane ATP synthase subunit C	27.64 9.85e-11 94-147
1137	PR00122A	Vacuolar ATP synthase 16kDa subunit signature I	10.78 6.00e-18 30-54
1137	PR00122B	Vacuolar ATP synthase 16kDa subunit signature II	10.11 4.32e-26 56-80
1137	PR00122C	Vacuolar ATP synthase 16kDa subunit signature III	10.28 9.40e-32 104-130
1137	PR00122D	Vacuolar ATP synthase 16kDa subunit signature IV	10.03 7.00e-28 131-154
1137	PR00124C	ATP synthase C subunit signature III	12.82 7.58e-11 128-153
1138	IPB002220A	Dihydrodipicolinate synthetase	16.79 9.29e-09 41-53
1138	IPB002220B	Dihydrodipicolinate synthetase	14.56 6.84e-14 68-89
1138	IPB002220C	Dihydrodipicolinate synthetase	25.64 1.23e-24 108-155
1138	IPB002220D	Dihydrodipicolinate synthetase	10.31 6.56e-10 164-175
1138	IPB002220F	Dihydrodipicolinate synthetase	12.81 6.14e-10 234-247

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SEQ ID NO:	Database entry ID	Description	Results*
1138	PR00146D	Dihydrodipicolinate synthase signature IV	14.98 9.79e-11 163-180
1139	IPB001734A	Sodium:solute symporter family	14.69 5.76e-16 51-67
1139	IPB001734B	Sodium:solute symporter family	18.26 6.63e-27 166-206
1139	IPB001734C	Sodium:solute symporter family	18.21 7.75e-23 924-953
1140	IPB000074C	Apolipoprotein A1/A4/E	22.23 1.58e-09 385-422
1140	IPB002607B	Hydratase/decarboxylase	29.50 3.64e-10 242-290
1140	PR00122B	Vacuolar ATP synthase 16kDa subunit signature II	10.11 7.56e-09 493-517
1142	IPB000897A	GTP-binding signal recognition particle (SRP54) domain	9.15 9.87e-09 611-630
1143	IPB000219A	Dbl domain (dbl/cdc24 rhoGEF family)	10.71 3.00e-09 156-165
1143	IPB000276C	Rhodopsin-like GPCR superfamily	8.03 1.41e-10 278-289
1143	IPB000276D	Rhodopsin-like GPCR superfamily	9.40 2.17e-10 324-340
1143	PR00237A	Rhodopsin-like GPCR superfamily signature I	9.81 8.92e-11 63-87
1143	PR00237B	Rhodopsin-like GPCR superfamily signature II	12.45 4.08e-09 96-117
1143	PR00237C	Rhodopsin-like GPCR superfamily signature III	14.77 5.50e-12 140-162
1143	PR00237E	Rhodopsin-like GPCR superfamily signature V	13.03 8.46e-09 226-249
1143	PR00237F	Rhodopsin-like GPCR superfamily signature VI	14.34 9.33e-13 268-292
1143	PR00237G	Rhodopsin-like GPCR superfamily signature VII	19.23 6.04e-15 314-340
1143	PR01157A	P2 purinoceptor signature I	9.05 3.52e-11 110-122
1144	PR00049D	Wilm's tumour protein signature IV	0.00 2.07e-09 7-21
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 1.10e-11 266-290
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 1.92e-11 265-289
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 2.23e-11 270-294
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 3.00e-09 262-286
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 3.25e-10 271-295
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 4.55e-09 272-296
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 5.09e-09 260-284
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 7.07e-10 267-291
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 7.09e-09 259-283
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 7.40e-12 268-292
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 8.63e-10 263-287
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 8.98e-11 269-293
1145	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 9.24e-12 264-288
1145	IPB000637B	HMG-I and HMG-Y DNA-binding domain	14.21 8.64e-09 272-290

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SEQ ID NO:	Database entry ID	Description	Results*
		(A+T-hook)	
1145	IPB001202B	WW / rsp5 / WWP domain	12.18 6.40e-15 387-401
1145	IPB001422C	Neuromodulin (GAP-43)	16.82 8.65e-09 258-293
1145	IPB001580F	Calreticulin family	2.93 8.65e-09 277-286
1145	PR00403A	WW domain signature I	19.41 5.03e-10 373-386
1145	PR00403B	WW domain signature II	13.50 5.33e-15 387-401
1148	PR00360B	C2 domain signature II	11.64 1.29e-11 279-292
1150	IPB000685G	Ribulose biphosphate carboxylase, large chain	10.38 5.23e-09 45-99
1150	PR01237A	Tumour necrosis factor c (lymphotoxin-beta) signature I	6.39 8.27e-09 38-61
1152	IPB000276A	Rhodopsin-like GPCR superfamily	11.56 7.63e-10 238-249
1152	PR00245A	Olfactory receptor signature I	10.98 1.30e-10 212-223
1152	PR00245B	Olfactory receptor signature II	13.73 5.50e-11 249-261
1152	PR00245C	Olfactory receptor signature III	14.65 6.87e-15 296-312
1152	PR00245E	Olfactory receptor signature V	8.96 2.04e-13 403-414
1152	PR00534A	Melanocortin receptor family signature I	12.77 7.52e-09 171-183
1153	IPB001680	G-protein beta WD-40 repeats	10.43 1.00e-11 456-467
1153	PR00320B	G protein beta WD-40 repeat signature II	12.82 7.55e-11 454-468
1153	PR00320C	G protein beta WD-40 repeat signature III	12.32 4.43e-11 454-468
1153	PR00962A	Lethal(2) giant larvae protein signature I	12.91 3.57e-22 17-35
1153	PR00962B	Lethal(2) giant larvae protein signature II	12.01 3.52e-29 310-332
1153	PR00962C	Lethal(2) giant larvae protein signature III	8.03 6.40e-23 362-382
1153	PR00962D	Lethal(2) giant larvae protein signature IV	9.91 4.16e-28 451-474
1153	PR00962E	Lethal(2) giant larvae protein signature V	8.81 3.67e-21 531-549
1153	PR00962F	Lethal(2) giant larvae protein signature VI	13.40 8.50e-24 568-587
1153	PR00962G	Lethal(2) giant larvae protein signature VII	14.51 6.54e-29 609-633
1153	PR00962H	Lethal(2) giant larvae protein signature VIII	13.53 3.53e-23 639-658
1153	PR00962I	Lethal(2) giant larvae protein signature IX	12.48 5.13e-23 708-727
1155	IPB002027A	Amino acid permease	18.88 8.82e-11 185-213
1155	IPB002027C	Amino acid permease	19.67 8.31e-21 385-423
1155	IPB002027D	Amino acid permease	22.00 6.79e-21 466-505
1157	PR01436C	NADH-ubiquinone oxidoreductase chain 2 signature III	9.53 7.75e-09 82-100
1158	IPB001428B	dUTPase	18.14 1.00e-14 107-125
1158	IPB001969A	Eukaryotic and viral aspartic protease active site	16.37 5.71e-09 195-211
1158	PR00783C	Major intrinsic protein family signature III	13.32 5.26e-17 31-50
1160	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 9.42e-10 1750-1760
1160	IPB000034A	Laminin B	22.21 1.85e-19 487-522
1160	IPB000034A	Laminin B	22.21 2.99e-10 1356-1391
1160	IPB000034A	Laminin B	22.21 3.84e-17 875-910
1160	IPB000034A	Laminin B	22.21 8.13e-10 1733-1768
1160	IPB000034A	Laminin B	22.21 8.56e-09 1263-1298
1160	IPB000034A	Laminin B	22.21 9.44e-09 533-568
1160	IPB000034B	Laminin B	21.22 1.23e-14 654-692
1160	IPB000034B	Laminin B	21.22 3.25e-31 1426-1464
1160	IPB000034B	Laminin B	21.22 3.33e-12 1287-1325
1160	IPB000034B	Laminin B	21.22 4.77e-10 1757-1795
1160	IPB000034B	Laminin B	21.22 4.99e-18 601-639
1160	IPB000034B	Laminin B	21.22 5.45e-09 511-549
1160	IPB000034C	Laminin B	12.97 3.09e-11 508-526
1160	IPB000034C	Laminin B	12.97 3.45e-09 319-337

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SEQ ID NO:	Database entry ID	Description	Results*
1160	IPB000034C	Laminin B	12.97 4.00e-11 443-461
1160	IPB000034C	Laminin B	12.97 4.05e-12 1377-1395
1160	IPB000034C	Laminin B	12.97 6.52e-13 554-572
1160	IPB000034C	Laminin B	12.97 6.56e-20 1754-1772
1160	IPB000034C	Laminin B	12.97 6.73e-09 1284-1302
1160	IPB000034C	Laminin B	12.97 8.01e-09 598-616
1160	IPB000034C	Laminin B	12.97 9.09e-11 651-669
1160	IPB000034C	Laminin B	12.97 9.31e-16 1653-1671
1160	IPB000561	EGF-like domain	4.89 5.50e-09 1754-1762
1160	IPB001001D	DNA polymerase III, beta chain	14.35 8.29e-09 2372-2395
1160	IPB001169K	Integrin beta, C-terminus	27.45 8.93e-11 1691-1733
1160	IPB001271	Mammalian defensin	19.97 5.91e-09 1728-1756
1160	IPB001774C	Delta serrate ligand	18.25 8.16e-09 545-587
1160	IPB001886A	Laminin N-terminal (Domain VI)	8.51 8.27e-09 124-131
1160	IPB001886B	Laminin N-terminal (Domain VI)	15.20 5.11e-21 286-308
1160	IPB001886C	Laminin N-terminal (Domain VI)	24.54 1.00e-09 1284-1323
1160	IPB001886C	Laminin N-terminal (Domain VI)	24.54 1.00e-11 1703-1742
1160	IPB001886C	Laminin N-terminal (Domain VI)	24.54 1.23e-10 508-547
1160	IPB001886C	Laminin N-terminal (Domain VI)	24.54 1.53e-14 1754-1793
1160	IPB001886C	Laminin N-terminal (Domain VI)	24.54 2.97e-33 319-358
1160	IPB001886C	Laminin N-terminal (Domain VI)	24.54 3.28e-13 391-430
1160	IPB001886C	Laminin N-terminal (Domain VI)	24.54 4.19e-10 554-593
1160	IPB001886C	Laminin N-terminal (Domain VI)	24.54 5.67e-10 1423-1462
1160	IPB001886C	Laminin N-terminal (Domain VI)	24.54 6.33e-11 598-637
1160	IPB001886C	Laminin N-terminal (Domain VI)	24.54 7.49e-10 1377-1416
1160	IPB001886C	Laminin N-terminal (Domain VI)	24.54 8.11e-11 651-690
1160	IPB001886D	Laminin N-terminal (Domain VI)	12.51 1.71e-09 439-457
1160	IPB001886D	Laminin N-terminal (Domain VI)	12.51 3.65e-17 1699-1717
1160	IPB001886D	Laminin N-terminal (Domain VI)	12.51 8.95e-10 1750-1768
1160	IPB001886D	Laminin N-terminal (Domain VI)	12.51 9.05e-22 387-405
1160	IPB001886E	Laminin N-terminal (Domain VI)	10.90 1.21e-13 1282-1298
1160	IPB001886E	Laminin N-terminal (Domain VI)	10.90 1.47e-09 317-333
1160	IPB001886E	Laminin N-terminal (Domain VI)	10.90 4.82e-16 1375-1391
1160	IPB001886E	Laminin N-terminal (Domain VI)	10.90 5.97e-09 649-665
1160	IPB001886E	Laminin N-terminal (Domain VI)	10.90 6.74e-09 441-457
1160	IPB001886E	Laminin N-terminal (Domain VI)	10.90 7.43e-13 1752-1768
1160	IPB001886E	Laminin N-terminal (Domain VI)	10.90 7.61e-11 596-612
1160	IPB001886E	Laminin N-terminal (Domain VI)	10.90 8.35e-11 506-522
1160	IPB001886E	Laminin N-terminal (Domain VI)	10.90 9.50e-20 552-568
1160	IPB003884C	Factor I membrane attack complex	13.00 3.22e-09 1403-1421
1160	PR00011A	Type III EGF-like signature I	14.05 1.68e-14 1416-1434
1160	PR00011A	Type III EGF-like signature I	14.05 1.69e-11 644-662
1160	PR00011A	Type III EGF-like signature I	14.05 3.88e-15 1277-1295
1160	PR00011A	Type III EGF-like signature I	14.05 3.93e-16 1370-1388
1160	PR00011A	Type III EGF-like signature I	14.05 3.95e-13 436-454
1160	PR00011A	Type III EGF-like signature I	14.05 5.00e-09 591-609
1160	PR00011A	Type III EGF-like signature I	14.05 5.05e-12 1318-1336
1160	PR00011A	Type III EGF-like signature I	14.05 5.43e-11 695-713
1160	PR00011A	Type III EGF-like signature I	14.05 6.82e-10 501-519
1160	PR00011A	Type III EGF-like signature I	14.05 8.83e-16 547-565
1160	PR00011B	Type III EGF-like signature II	13.08 1.00e-09 591-609
1160	PR00011B	Type III EGF-like signature II	13.08 1.66e-10 695-713
1160	PR00011B	Type III EGF-like signature II	13.08 4.18e-11 644-662

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SEQ ID NO:	Database entry ID	Description	Results*
1160	PR00011B	Type III EGF-like signature II	13.08 4.35e-15 1370-1388
1160	PR00011B	Type III EGF-like signature II	13.08 5.57e-12 436-454
1160	PR00011B	Type III EGF-like signature II	13.08 5.71e-17 547-565
1160	PR00011B	Type III EGF-like signature II	13.08 6.46e-12 1416-1434
1160	PR00011B	Type III EGF-like signature II	13.08 7.52e-13 1277-1295
1160	PR00011B	Type III EGF-like signature II	13.08 8.48e-11 1318-1336
1160	PR00011C	Type III EGF-like signature III	25.79 2.62e-09 651-679
1160	PR00011C	Type III EGF-like signature III	25.79 6.53e-10 1423-1451
1160	PR00011D	Type III EGF-like signature IV	12.12 1.18e-14 1370-1388
1160	PR00011D	Type III EGF-like signature IV	12.12 3.63e-10 695-713
1160	PR00011D	Type III EGF-like signature IV	12.12 4.96e-14 501-519
1160	PR00011D	Type III EGF-like signature IV	12.12 6.01e-09 591-609
1160	PR00011D	Type III EGF-like signature IV	12.12 7.65e-10 644-662
1160	PR00011D	Type III EGF-like signature IV	12.12 8.25e-17 547-565
1160	PR00011D	Type III EGF-like signature IV	12.12 8.33e-13 436-454
1160	PR00011D	Type III EGF-like signature IV	12.12 8.92e-14 1416-1434
1160	PR00011D	Type III EGF-like signature IV	12.12 9.17e-13 1277-1295
1160	PR00011D	Type III EGF-like signature IV	12.12 9.23e-09 1747-1765
1160	PR00877D	Plant PEC family metallothionein signature IV	6.45 1.89e-09 1308-1315
1161	IPB000034C	Laminin B	12.97 6.42e-10 205-223
1161	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 1.00e-10 158-173
1161	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 9.29e-09 196-211
1161	IPB000359A	Cystine-knot domain	23.24 4.86e-10 129-153
1161	IPB000561	EGF-like domain	4.89 9.25e-10 46-54
1161	IPB001762A	Disintegrin	23.93 9.65e-09 95-135
1161	IPB001774C	Delta serrate ligand	18.25 1.71e-31 37-79
1161	IPB001774C	Delta serrate ligand	18.25 9.17e-12 68-110
1161	IPB001862F	Membrane attack complex components/perforin/complement C9	29.39 2.65e-09 170-217
1161	IPB001862F	Membrane attack complex components/perforin/complement C9	29.39 8.53e-09 132-179
1161	IPB001886E	Laminin N-terminal (Domain VI)	10.90 9.67e-10 44-60
1161	PR00010A	Type II EGF-like signature I	12.91 1.27e-09 143-154
1161	PR00010C	Type II EGF-like signature III	6.98 2.54e-09 163-173
1161	PR00011A	Type III EGF-like signature I	14.05 6.88e-09 39-57
1161	PR00011B	Type III EGF-like signature II	13.08 7.88e-10 39-57
1161	PR00011D	Type III EGF-like signature IV	12.12 4.57e-12 39-57
1161	PR01217G	Proline rich extensin signature VII	4.02 7.79e-09 221-246
1162	IPB000471A	Interferon alpha, beta and delta family	27.36 2.86e-34 45-98
1162	PR00266A	Interferon alpha and beta subunit signature I	13.41 9.59e-14 67-79
1163	IPB000975D	Interleukin-1	24.45 5.55e-09 59-98
1163	IPB000975E	Interleukin-1	28.12 9.80e-09 103-142
1163	PR00264A	Interleukin-1 precursor family signature I	18.63 1.00e-08 62-82
1163	PR01360C	Interleukin-1 receptor antagonist precursor IL-1RA signature III	10.33 4.84e-11 65-82
1163	PR01360F	Interleukin-1 receptor antagonist precursor IL-1RA signature VI	14.44 3.11e-12 124-142
1164	IPB000072	Platelet-derived growth factor (PDGF)	13.51 4.00e-26 75-97
1164	IPB003498F	Probable DNA packing protein, C-terminus	23.31 7.55e-09 154-193
1165	IPB000975E	Interleukin-1	28.12 3.57e-12 95-134
1165	PR00264A	Interleukin-1 precursor family signature I	18.63 9.85e-09 55-75

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SEQ ID NO:	Database entry ID	Description	Results*
1165	PR00264C	Interleukin-1 precursor family signature III	19.37 4.90e-16 108-123
1165	PR01357F	Interleukin-1 alpha/beta precursor family signature VI	17.87 7.15e-10 108-123
1165	PR01360E	Interleukin-1 receptor antagonist precursor IL-1RA signature V	9.69 9.33e-13 95-115
1165	PR01360F	Interleukin-1 receptor antagonist precursor IL-1RA signature VI	14.44 9.86e-18 116-134
1166	IPB000276C	Rhodopsin-like GPCR superfamily	8.03 6.50e-11 33-44
1166	PR00237F	Rhodopsin-like GPCR superfamily signature VI	14.34 5.05e-16 23-47
1166	PR00237G	Rhodopsin-like GPCR superfamily signature VII	19.23 8.80e-13 70-96
1166	PR00427E	Interleukin-8 receptor signature V	7.33 3.84e-17 6-21
1166	PR00427F	Interleukin-8 receptor signature VI	12.53 2.63e-12 48-64
1166	PR00427G	Interleukin-8 receptor signature VII	10.47 8.53e-17 98-114
1166	PR00573D	Interleukin 8B receptor signature IV	15.06 1.85e-18 114-129
1167	PR00414A	Palmitoyl protein thioesterase signature I	10.61 3.44e-31 26-48
1167	PR00414B	Palmitoyl protein thioesterase signature II	11.87 6.79e-25 66-85
1167	PR00414C	Palmitoyl protein thioesterase signature III	13.39 1.90e-23 106-122
1167	PR00414D	Palmitoyl protein thioesterase signature IV	17.22 2.13e-27 151-170
1167	PR00414E	Palmitoyl protein thioesterase signature V	17.10 1.43e-27 185-204
1167	PR00414G	Palmitoyl protein thioesterase signature VII	12.98 2.36e-24 258-276
1168	IPB000215A	Serpins	13.01 4.18e-20 73-96
1168	IPB000215B	Serpins	9.87 9.68e-09 181-193
1168	IPB000215C	Serpins	13.90 7.11e-11 208-222
1168	IPB000215D	Serpins	15.35 3.88e-16 310-336
1168	IPB000215E	Serpins	15.36 1.56e-18 391-415
1170	IPB001271	Mammalian defensin	19.97 3.42e-21 103-131
1172	IPB000387	Tyrosine specific protein phosphatase and dual specificity protein phosphatase family	10.77 5.85e-13 439-449
1172	PR00700A	Protein tyrosine phosphatase signature I	6.05 1.00e-10 295-302
1172	PR00700B	Protein tyrosine phosphatase signature II	17.06 5.70e-21 313-333
1172	PR00700C	Protein tyrosine phosphatase signature III	13.89 9.05e-16 399-416
1172	PR00700D	Protein tyrosine phosphatase signature IV	12.83 7.84e-19 436-454
1172	PR00700E	Protein tyrosine phosphatase signature V	16.60 1.93e-10 467-482
1172	PR00700F	Protein tyrosine phosphatase signature VI	10.33 1.00e-11 483-493
1172	PR01371E	Salmonella/Yersinia modular tyrosine phosphatase signature V	11.71 2.11e-09 437-448
1187	IPB000008C	C2 domain	23.37 2.44e-09 61-100
1187	IPB002642A	Lysophospholipase catalytic domain	18.37 1.69e-13 355-380
1187	IPB002642B	Lysophospholipase catalytic domain	11.84 4.38e-15 383-407
1187	IPB002642E	Lysophospholipase catalytic domain	18.19 6.91e-10 509-534
1187	IPB002642G	Lysophospholipase catalytic domain	34.11 6.72e-10 678-726
1187	PR00360B	C2 domain signature II	11.64 8.67e-12 88-101
1188	PR00860B	Vertebrate metallothionein signature II	6.90 7.18e-09 52-65
1189	IPB000566B	Lipocalin and cytosolic fatty-acid binding protein	8.91 9.53e-09 122-132
1189	IPB002223	Pancreatic trypsin inhibitor (Kunitz) family	17.66 1.32e-23 285-319
1189	IPB002223	Pancreatic trypsin inhibitor (Kunitz) family	17.66 9.12e-15 247-281
1189	PR00179A	Lipocalin signature I	13.97 2.13e-10 38-50
1189	PR00179B	Lipocalin signature II	7.67 4.91e-12 122-134
1189	PR00179C	Lipocalin signature III	17.26 4.60e-09 150-165
1189	PR00759A	Basic protease (Kunitz-type) inhibitor family signature I	14.67 5.88e-09 228-242

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SEQ ID NO:	Database entry ID	Description	Results*
1189	PR00759B	Basic protease (Kunitz-type) inhibitor family signature II	12.35 3.81e-10 294-304
1189	PR00759B	Basic protease (Kunitz-type) inhibitor family signature II	12.35 8.71e-12 256-266
1189	PR00759C	Basic protease (Kunitz-type) inhibitor family signature III	12.43 6.00e-14 304-319
1189	PR01215A	Alpha-1-microglobulin signature I	14.08 3.25e-18 32-45
1189	PR01215B	Alpha-1-microglobulin signature II	14.28 7.00e-15 47-58
1189	PR01215C	Alpha-1-microglobulin signature III	8.22 3.63e-19 91-106
1189	PR01215D	Alpha-1-microglobulin signature IV	12.88 1.53e-27 113-132
1189	PR01215E	Alpha-1-microglobulin signature V	12.83 1.66e-24 145-166
1189	PR01215F	Alpha-1-microglobulin signature VI	10.31 9.59e-25 173-192
1189	PR01273A	Invertebrate colouration protein signature I	14.08 3.53e-09 33-49
1200	IPB001594	DHHC-type Zn-finger	23.81 7.47e-31 99-143
1201	IPB001909	KRAB box	17.37 9.61e-26 35-69
1202	IPB001909	KRAB box	17.37 9.61e-26 35-69
1203	IPB000961A	Protein kinase C-terminal domain	16.82 5.97e-09 74-108
1204	IPB000001D	Kringle	11.31 3.92e-15 81-97
1204	IPB000126A	Serine proteases, V8 family	11.75 9.51e-12 81-96
1204	IPB000177K	Apple domain	13.19 3.55e-11 83-115
1204	IPB001254A	Serine proteases, trypsin family	9.98 6.06e-18 81-97
1204	PR00722A	Chymotrypsin serine protease family (S1) signature I	12.06 3.37e-17 82-97
1208	PR00179B	Lipocalin signature II	7.67 7.30e-09 121-133
1208	PR01174F	Retinol binding protein signature VI	11.76 9.34e-09 120-136
1208	PR01254A	Prostaglandin D synthase signature I	12.32 9.79e-09 31-54
1208	PR01275B	Neutrophil gelatinase lipocalin signature II	9.02 3.16e-11 39-49
1209	IPB001007C	von Willebrand factor, type C repeat	20.89 5.97e-10 34-55
1212	PR00019A	Leucine-rich repeat signature I	11.72 2.50e-12 177-190
1212	PR00019A	Leucine-rich repeat signature I	11.72 7.82e-09 390-403
1212	PR00019B	Leucine-rich repeat signature II	11.42 1.64e-13 174-187
1212	PR00019B	Leucine-rich repeat signature II	11.42 9.18e-11 387-400
1213	IPB000834B	Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family	13.51 2.50e-17 103-117
1213	IPB000834C	Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family	17.20 2.80e-15 172-188
1213	IPB000834D	Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family	18.95 4.72e-12 199-225
1213	IPB000834E	Zinc carboxypeptidases, carboxypeptidase A metalloprotease (M14) family	9.80 2.15e-09 228-242
1213	PR00765B	Carboxypeptidase A metalloprotease (M14) family signature II	14.48 1.39e-15 99-113
1213	PR00765C	Carboxypeptidase A metalloprotease (M14) family signature III	10.88 1.82e-10 179-187
1213	PR00765D	Carboxypeptidase A metalloprotease (M14) family signature IV	14.06 9.45e-12 233-246
1214	PR01536C	Interleukin-1 receptor type I and type II family signature III	19.92 7.00e-09 67-90
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 1.30e-11 56-93
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 2.22e-15 44-81
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 2.29e-19 38-75
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 2.74e-09 20-57
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 2.82e-15 68-105
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 3.05e-10 92-129

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SEQ ID NO:	Database entry ID	Description	Results*
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 3.22e-11 26-63
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 3.34e-14 89-126
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 3.36e-12 32-69
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 3.57e-14 47-84
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 4.16e-15 71-108
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 4.17e-16 80-117
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 4.28e-15 41-78
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 4.62e-14 65-102
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 4.65e-15 50-87
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 5.56e-13 62-99
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 5.56e-14 83-120
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 5.91e-14 29-66
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 7.07e-10 95-132
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 7.46e-16 86-123
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 7.59e-16 77-114
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 8.29e-12 53-90
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 8.36e-14 59-96
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 9.00e-19 35-72
1221	IPB000885A	Fibrillar collagen C-terminal domain	11.46 9.42e-14 74-111
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 1.00e-20 72-125
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 1.22e-16 33-86
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 1.47e-18 51-104
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 1.51e-21 69-122
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 1.74e-20 36-89
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 1.94e-10 90-143
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 1.98e-09 15-68
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 2.21e-14 27-80
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 3.03e-17 78-131
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 3.22e-15 24-77
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 3.84e-13 84-137
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 3.95e-24 42-95
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 4.16e-18 30-83
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 4.32e-23 75-128
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 4.70e-20 60-113
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 5.07e-20 45-98
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 6.40e-09 3-56
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 6.61e-18 63-116
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 7.62e-22 57-110
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 7.63e-09 9-62
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 7.71e-09 12-65
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 7.81e-21 39-92
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 7.84e-19 66-119
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 7.95e-13 18-71
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 8.89e-10 93-146
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 9.07e-22 54-107
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 9.16e-12 81-134
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 9.41e-13 21-74
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 9.88e-20 48-101
1221	IPB000885B	Fibrillar collagen C-terminal domain	19.15 9.91e-12 87-140
1221	IPB001073A	Complement C1q protein	22.14 1.00e-11 40-74
1221	IPB001073A	Complement C1q protein	22.14 1.42e-09 55-89
1221	IPB001073A	Complement C1q protein	22.14 1.67e-11 79-113
1221	IPB001073A	Complement C1q protein	22.14 2.97e-09 43-77

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SEQ ID NO:	Database entry ID	Description	Results*
1221	IPB001073A	Complement C1q protein	22.14 3.39e-09 91-125
1221	IPB001073A	Complement C1q protein	22.14 3.75e-10 31-65
1221	IPB001073A	Complement C1q protein	22.14 4.09e-09 85-119
1221	IPB001073A	Complement C1q protein	22.14 4.45e-13 34-68
1221	IPB001073A	Complement C1q protein	22.14 4.60e-12 94-128
1221	IPB001073A	Complement C1q protein	22.14 5.50e-11 88-122
1221	IPB001073A	Complement C1q protein	22.14 5.67e-11 76-110
1221	IPB001073A	Complement C1q protein	22.14 7.10e-10 52-86
1221	IPB001073A	Complement C1q protein	22.14 7.33e-11 82-116
1221	IPB001073A	Complement C1q protein	22.14 7.51e-13 37-71
1221	IPB001073A	Complement C1q protein	22.14 7.83e-11 97-131
1221	IPB001073A	Complement C1q protein	22.14 8.17e-10 58-92
1221	IPB001073A	Complement C1q protein	22.14 8.59e-09 49-83
1221	IPB001073A	Complement C1q protein	22.14 9.81e-13 100-134
1221	IPB001073B	Complement C1q protein	20.88 7.75e-28 150-184
1221	IPB001073C	Complement C1q protein	13.07 8.56e-16 214-233
1221	IPB001073D	Complement C1q protein	7.60 7.68e-09 251-260
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 1.09e-13 82-134
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 1.39e-09 91-143
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 1.42e-16 64-116
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 2.41e-17 31-83
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 2.47e-16 76-128
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 2.73e-17 67-119
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 2.89e-20 49-101
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 3.97e-09 10-62
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 4.03e-16 79-131
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 4.79e-20 46-98
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 4.80e-17 25-77
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 4.80e-17 28-80
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 4.82e-21 40-92
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 4.96e-12 13-65
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 5.85e-09 88-140
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 6.56e-18 34-86
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 6.77e-14 22-74
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 7.39e-23 37-89
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 7.55e-14 16-68

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
		4 procollagen	
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 7.99e-20 70-122
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 8.07e-22 43-95
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 8.30e-23 61-113
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 8.58e-20 58-110
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 9.09e-15 19-71
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 9.18e-19 55-107
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 9.37e-12 85-137
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 9.56e-18 73-125
1221	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 9.59e-24 52-104
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 1.00e-11 104-124
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 1.49e-09 47-67
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 1.85e-09 107-127
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 2.82e-09 41-61
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 2.82e-09 86-106
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 3.31e-09 71-91
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 3.55e-09 56-76
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 3.68e-09 50-70
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 3.92e-09 68-88
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 5.14e-09 89-109
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 5.24e-10 101-121
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 6.01e-10 38-58
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 6.72e-09 59-79
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 7.81e-09 35-55
1221	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 9.15e-09 44-64
1221	PR00007A	Complement C1Q domain signature I	20.64 7.47e-17 143-169
1221	PR00007B	Complement C1Q domain signature II	15.63 5.26e-14 170-189
1221	PR00007C	Complement C1Q domain signature III	16.13 2.07e-14 214-235
1221	PR00007D	Complement C1Q domain signature IV	9.66 3.91e-10 249-259
1223	IPB000053H	Thymidine/pyrimidine-nucleoside	12.28 9.76e-09 28-37

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
		phosphorylase	
1223	IPB000095E	PAK-box /P21-Rho-binding	17.62 4.19e-11 275-320
1223	IPB000494C	Epidermal growth-factor receptor (EGFR), L domain	24.40 3.60e-31 261-307
1223	IPB000494D	Epidermal growth-factor receptor (EGFR), L domain	19.44 7.50e-29 322-371
1223	IPB000494E	Epidermal growth-factor receptor (EGFR), L domain	21.65 2.46e-24 379-414
1223	IPB000861F	PKN/rhopilin/rhotekin rho-binding repeat	16.50 3.15e-11 268-322
1223	IPB000959B	POLO box duplicated region	15.68 1.99e-10 251-291
1223	IPB000961C	Protein kinase C-terminal domain	15.48 6.29e-13 274-308
1223	IPB001245A	Tyrosine kinase catalytic domain	22.45 7.19e-26 267-307
1223	IPB001245B	Tyrosine kinase catalytic domain	21.68 5.24e-23 325-363
1223	IPB001359H	Synapsin	22.58 3.51e-10 803-853
1223	IPB001359H	Synapsin	22.58 6.85e-09 777-827
1223	IPB001772C	Kinase associated domain 1	20.66 7.93e-13 262-292
1223	IPB003306E	WIF domain	25.51 5.35e-12 379-424
1223	IPB003527C	MAP kinase	14.70 2.48e-14 259-307
1223	PR00109A	Tyrosine kinase catalytic domain signature I	12.56 5.14e-10 237-250
1223	PR00109B	Tyrosine kinase catalytic domain signature II	11.07 2.61e-18 274-292
1223	PR00109C	Tyrosine kinase catalytic domain signature III	11.86 1.87e-10 324-334
1223	PR00109D	Tyrosine kinase catalytic domain signature IV	17.61 7.12e-21 343-365
1223	PR00109E	Tyrosine kinase catalytic domain signature V	12.99 5.09e-20 388-410
1223	PR01217B	Proline rich extensin signature II	4.82 6.09e-09 927-943
1224	PR00453A	Von Willebrand factor type A domain signature I	11.78 3.15e-09 50-67
1225	IPB000734	Lipase	10.25 8.13e-09 164-178
1227	IPB001304A	C-type lectin domain	17.98 3.48e-10 41-65
1227	IPB001304B	C-type lectin domain	10.18 5.95e-09 99-111
1227	PR01504F	Pancreatitis-associated protein signature VI	12.72 6.45e-09 153-167
1237	IPB002181A	Fibrinogen beta and gamma chains C-terminal globular domain	18.44 2.32e-10 244-260
1237	IPB002181B	Fibrinogen beta and gamma chains C-terminal globular domain	20.16 9.57e-10 271-307
1237	IPB002181C	Fibrinogen beta and gamma chains C-terminal globular domain	15.87 1.00e-08 294-306
1237	IPB002181D	Fibrinogen beta and gamma chains C-terminal globular domain	29.18 5.14e-19 312-352
1257	IPB000483	Leucine rich repeat C-terminal domain	11.18 1.58e-09 423-437
1257	PR00019B	Leucine-rich repeat signature II	11.42 8.33e-10 124-137
1257	PR00019B	Leucine-rich repeat signature II	11.42 8.33e-10 316-329
1263	IPB001762A	Disintegrin	23.93 6.45e-17 434-474
1263	IPB001762A	Disintegrin	23.93 6.47e-09 416-456
1263	IPB002870A	Reprolysin family propeptide	12.22 3.31e-10 63-79
1263	IPB002870B	Reprolysin family propeptide	24.73 6.56e-14 109-147
1263	IPB002870E	Reprolysin family propeptide	11.90 2.50e-11 341-353
1263	PR00289A	Disintegrin signature I	14.29 2.65e-13 450-469
1263	PR00873D	Echinoidea (sea urchin) metallothionein signature IV	8.25 7.35e-09 608-626
1264	IPB002168A	Lipolytic enzymes	11.40 5.07e-11 139-153

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SEQ ID NO:	Database entry ID	Description	Results*
1264	IPB002168B	Lipolytic enzymes	30.88 5.14e-19 157-204
1264	IPB002168C	Lipolytic enzymes	9.77 4.00e-16 216-229
1264	IPB002168D	Lipolytic enzymes	19.85 6.70e-18 369-393
1264	IPB002469I	Dipeptidyl peptidase IV, N-terminus	10.99 6.29e-09 211-229
1264	PR01040B	Tyrosyl-tRNA synthetase signature II	14.69 7.00e-09 245-260
1266	IPB000753A	Clusterin	12.20 6.45e-18 2-16
1266	IPB000753B	Clusterin	11.42 1.00e-40 39-83
1266	IPB000753D	Clusterin	15.34 1.00e-40 163-204
1266	IPB000753E	Clusterin	13.24 1.00e-40 230-279
1266	IPB000753F	Clusterin	17.89 1.00e-40 310-361
1266	IPB000753G	Clusterin	17.73 9.55e-24 372-390
1267	IPB000215A	Serpins	13.01 9.14e-18 107-130
1267	IPB000215C	Serpins	13.90 7.88e-15 211-225
1267	IPB000215D	Serpins	15.35 3.74e-17 314-340
1267	IPB000215E	Serpins	15.36 6.68e-16 401-425
1268	IPB000215A	Serpins	13.01 9.14e-18 125-148
1268	IPB000215B	Serpins	9.87 1.82e-11 218-230
1268	IPB000215C	Serpins	13.90 7.88e-15 247-261
1268	IPB000215D	Serpins	15.35 3.74e-17 350-376
1268	IPB000215E	Serpins	15.36 7.19e-18 437-461
1273	IPB001307A	Rhodanese signatures	11.98 8.64e-10 10-20
1273	IPB001307B	Rhodanese signatures	16.09 3.89e-14 48-61
1273	IPB001307C	Rhodanese signatures	15.11 1.28e-15 82-101
1273	IPB001307D	Rhodanese signatures	15.87 4.00e-26 110-135
1273	IPB001307E	Rhodanese signatures	13.19 5.36e-10 180-191
1273	IPB001307G	Rhodanese signatures	11.73 9.31e-16 251-263
1274	IPB000001D	Kringle	11.31 4.95e-14 147-163
1274	IPB000001G	Kringle	29.29 4.46e-11 259-287
1274	IPB000001H	Kringle	12.24 2.80e-10 299-309
1274	IPB000126A	Serine proteases, V8 family	11.75 9.25e-10 147-162
1274	IPB000177K	Apple domain	13.19 2.18e-11 149-181
1274	IPB000177L	Apple domain	11.33 9.92e-10 178-216
1274	IPB000177N	Apple domain	10.17 5.19e-24 289-323
1274	IPB000177O	Apple domain	14.39 9.00e-16 324-352
1274	IPB001254A	Serine proteases, trypsin family	9.98 3.37e-16 147-163
1274	IPB001254B	Serine proteases, trypsin family	15.01 5.50e-16 297-320
1274	IPB001254C	Serine proteases, trypsin family	16.54 4.86e-20 327-346
1274	IPB002093D	BRCA2 repeat	8.99 9.77e-09 8-46
1274	PR00722A	Chymotrypsin serine protease family (S1) signature I	12.06 3.88e-15 148-163
1274	PR00722B	Chymotrypsin serine protease family (S1) signature II	12.69 3.74e-09 203-217
1274	PR00722C	Chymotrypsin serine protease family (S1) signature III	10.74 1.69e-14 296-308
1279	PR00704I	Calpain cysteine protease (C2) family signature IX	9.42 4.14e-14 145-173
1284	IPB001706	Ribosomal protein L35	21.01 1.00e-18 119-157
1285	IPB001706	Ribosomal protein L35	21.01 1.00e-18 119-157
1287	IPB000822	Zinc finger, C2H2 type	14.67 1.43e-11 399-424
1287	IPB000822	Zinc finger, C2H2 type	14.67 2.50e-20 259-284
1287	IPB000822	Zinc finger, C2H2 type	14.67 3.25e-19 231-256
1287	IPB000822	Zinc finger, C2H2 type	14.67 5.50e-19 343-368
1287	IPB000822	Zinc finger, C2H2 type	14.67 6.54e-18 203-228

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SEQ ID NO:	Database entry ID	Description	Results*
1287	IPB000822	Zinc finger, C2H2 type	14.67 8.50e-13 315-340
1287	IPB000822	Zinc finger, C2H2 type	14.67 8.62e-18 287-312
1287	IPB000822	Zinc finger, C2H2 type	14.67 9.10e-22 175-200
1287	IPB000822	Zinc finger, C2H2 type	14.67 9.10e-22 371-396
1287	IPB001275	DM DNA binding domain	19.17 2.75e-12 359-398
1287	IPB001275	DM DNA binding domain	19.17 3.57e-11 275-314
1287	IPB001275	DM DNA binding domain	19.17 4.34e-11 191-230
1287	IPB001275	DM DNA binding domain	19.17 9.60e-12 247-286
1287	IPB001275	DM DNA binding domain	19.17 9.87e-12 331-370
1287	IPB001909	KRAB box	17.37 3.33e-22 16-50
1287	PR00048A	C2H2-type zinc finger signature I	9.94 2.59e-12 396-409
1287	PR00048A	C2H2-type zinc finger signature I	9.94 2.88e-09 340-353
1287	PR00048A	C2H2-type zinc finger signature I	9.94 3.77e-14 368-381
1287	PR00048A	C2H2-type zinc finger signature I	9.94 5.15e-14 284-297
1287	PR00048A	C2H2-type zinc finger signature I	9.94 6.63e-09 312-325
1287	PR00048A	C2H2-type zinc finger signature I	9.94 6.73e-10 256-269
1287	PR00048A	C2H2-type zinc finger signature I	9.94 9.36e-13 200-213
1287	PR00048B	C2H2-type zinc finger signature II	5.52 1.00e-12 188-197
1287	PR00048B	C2H2-type zinc finger signature II	5.52 3.25e-11 384-393
1287	PR00048B	C2H2-type zinc finger signature II	5.52 4.00e-09 356-365
1287	PR00048B	C2H2-type zinc finger signature II	5.52 4.86e-10 244-253
1287	PR00048B	C2H2-type zinc finger signature II	5.52 5.50e-09 300-309
1287	PR00048B	C2H2-type zinc finger signature II	5.52 7.00e-12 272-281
1292	IPB000034C	Laminin B	12.97 7.31e-09 54-72
1292	IPB000561	EGF-like domain	4.89 8.07e-09 54-62
1292	IPB001774D	Delta serrate ligand	19.23 5.91e-09 20-66
1294	IPB001007B	von Willebrand factor, type C repeat	10.03 2.89e-09 92-101
1295	IPB000822	Zinc finger, C2H2 type	14.67 1.00e-18 433-458
1295	IPB000822	Zinc finger, C2H2 type	14.67 1.00e-22 405-430
1295	IPB000822	Zinc finger, C2H2 type	14.67 1.90e-22 321-346
1295	IPB000822	Zinc finger, C2H2 type	14.67 4.00e-10 265-290
1295	IPB000822	Zinc finger, C2H2 type	14.67 4.86e-10 489-514
1295	IPB000822	Zinc finger, C2H2 type	14.67 6.25e-19 377-402
1295	IPB000822	Zinc finger, C2H2 type	14.67 7.75e-20 461-486
1295	IPB000822	Zinc finger, C2H2 type	14.67 8.50e-19 349-374
1295	IPB001222	TFIIIS zinc ribbon domain	24.63 3.66e-09 433-469
1295	IPB001275	DM DNA binding domain	19.17 3.85e-09 309-348
1295	IPB001275	DM DNA binding domain	19.17 4.77e-10 337-376
1295	IPB001275	DM DNA binding domain	19.17 5.22e-09 421-460
1295	IPB001275	DM DNA binding domain	19.17 8.42e-10 393-432
1295	IPB001275	DM DNA binding domain	19.17 9.27e-10 449-488
1295	IPB001909	KRAB box	17.37 9.50e-32 10-44
1295	PR00048A	C2H2-type zinc finger signature I	9.94 1.00e-10 318-331
1295	PR00048A	C2H2-type zinc finger signature I	9.94 1.00e-13 402-415
1295	PR00048A	C2H2-type zinc finger signature I	9.94 1.64e-13 346-359
1295	PR00048A	C2H2-type zinc finger signature I	9.94 5.76e-12 374-387
1295	PR00048A	C2H2-type zinc finger signature I	9.94 5.85e-14 458-471
1295	PR00048A	C2H2-type zinc finger signature I	9.94 7.92e-14 486-499
1295	PR00048A	C2H2-type zinc finger signature I	9.94 8.62e-14 430-443
1295	PR00048B	C2H2-type zinc finger signature II	5.52 1.50e-09 418-427
1295	PR00048B	C2H2-type zinc finger signature II	5.52 3.50e-09 474-483
1295	PR00048B	C2H2-type zinc finger signature II	5.52 6.79e-10 334-343
1295	PR00048B	C2H2-type zinc finger signature II	5.52 8.50e-09 390-399

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1296	IPB000822	Zinc finger, C2H2 type	14.67 1.69e-18 304-329
1296	IPB000822	Zinc finger, C2H2 type	14.67 3.25e-14 444-469
1296	IPB000822	Zinc finger, C2H2 type	14.67 3.77e-18 220-245
1296	IPB000822	Zinc finger, C2H2 type	14.67 6.25e-19 248-273
1296	IPB000822	Zinc finger, C2H2 type	14.67 6.73e-21 416-441
1296	IPB000822	Zinc finger, C2H2 type	14.67 7.00e-20 276-301
1296	IPB000822	Zinc finger, C2H2 type	14.67 8.20e-16 388-413
1296	IPB000822	Zinc finger, C2H2 type	14.67 8.20e-23 192-217
1296	IPB000822	Zinc finger, C2H2 type	14.67 8.36e-21 332-357
1296	IPB000822	Zinc finger, C2H2 type	14.67 8.50e-19 472-497
1296	IPB000822	Zinc finger, C2H2 type	14.67 8.62e-18 500-525
1296	IPB000822	Zinc finger, C2H2 type	14.67 9.18e-21 360-385
1296	IPB001275	DM DNA binding domain	19.17 1.97e-10 488-527
1296	IPB001275	DM DNA binding domain	19.17 2.37e-09 376-415
1296	IPB001275	DM DNA binding domain	19.17 2.95e-10 264-303
1296	IPB001275	DM DNA binding domain	19.17 3.96e-09 236-275
1296	IPB001275	DM DNA binding domain	19.17 5.10e-09 432-471
1296	IPB001275	DM DNA binding domain	19.17 5.38e-10 208-247
1296	IPB001275	DM DNA binding domain	19.17 5.50e-10 404-443
1296	IPB001275	DM DNA binding domain	19.17 5.76e-11 460-499
1296	IPB001275	DM DNA binding domain	19.17 5.90e-09 180-219
1296	IPB001275	DM DNA binding domain	19.17 6.79e-11 348-387
1296	IPB001275	DM DNA binding domain	19.17 8.30e-10 320-359
1296	IPB001909	KRAB box	17.37 5.50e-37 16-50
1296	PR00048A	C2H2-type zinc finger signature I	9.94 1.38e-09 217-230
1296	PR00048A	C2H2-type zinc finger signature I	9.94 2.06e-12 245-258
1296	PR00048A	C2H2-type zinc finger signature I	9.94 2.06e-12 301-314
1296	PR00048A	C2H2-type zinc finger signature I	9.94 3.86e-10 273-286
1296	PR00048A	C2H2-type zinc finger signature I	9.94 4.71e-12 413-426
1296	PR00048A	C2H2-type zinc finger signature I	9.94 4.86e-13 329-342
1296	PR00048A	C2H2-type zinc finger signature I	9.94 5.50e-15 385-398
1296	PR00048A	C2H2-type zinc finger signature I	9.94 5.50e-15 469-482
1296	PR00048A	C2H2-type zinc finger signature I	9.94 5.91e-10 497-510
1296	PR00048A	C2H2-type zinc finger signature I	9.94 6.14e-13 189-202
1296	PR00048A	C2H2-type zinc finger signature I	9.94 6.14e-13 525-538
1296	PR00048A	C2H2-type zinc finger signature I	9.94 6.82e-12 357-370
1296	PR00048B	C2H2-type zinc finger signature II	5.52 1.00e-10 261-270
1296	PR00048B	C2H2-type zinc finger signature II	5.52 1.00e-10 289-298
1296	PR00048B	C2H2-type zinc finger signature II	5.52 2.29e-10 205-214
1296	PR00048B	C2H2-type zinc finger signature II	5.52 4.86e-10 513-522
1296	PR00048B	C2H2-type zinc finger signature II	5.52 5.50e-10 317-326
1296	PR00048B	C2H2-type zinc finger signature II	5.52 5.50e-10 485-494
1296	PR00048B	C2H2-type zinc finger signature II	5.52 5.50e-11 345-354
1296	PR00048B	C2H2-type zinc finger signature II	5.52 6.79e-10 233-242
1296	PR00048B	C2H2-type zinc finger signature II	5.52 7.75e-11 429-438
1299	IPB000130	Neutral zinc metalloproteases, zinc-binding region	5.86 1.00e-11 188-198
1299	IPB001818B	Matrixin	26.48 4.63e-13 87-128
1299	IPB001818C	Matrixin	24.38 4.54e-09 134-179
1299	IPB001818D	Matrixin	14.91 3.36e-25 182-213
1299	IPB001818E	Matrixin	8.86 4.26e-10 222-235
1299	IPB002870E	Reprolysins family propeptide	11.90 2.00e-09 190-202
1299	PR00138A	Matrixin signature I	12.54 9.25e-10 37-50

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1299	PR00138B	Matrixin signature II	14.84 4.51e-11 106-121
1299	PR00138C	Matrixin signature III	20.07 8.86e-11 132-160
1299	PR00138D	Matrixin signature IV	14.57 1.86e-21 188-213
1299	PR00138E	Matrixin signature V	7.10 9.77e-11 222-235
1299	PR00480B	Astacin family signature II	14.35 1.14e-09 183-201
1301	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 6.09e-11 150-187
1305	IPB002579C	Domain of unknown function DUF25	13.50 3.89e-28 75-102
1305	IPB002579D	Domain of unknown function DUF25	11.55 7.92e-12 128-139
1305	IPB002579E	Domain of unknown function DUF25	12.14 9.31e-13 149-159
1307	IPB002350	Kazal-type serine protease inhibitor family	31.78 4.09e-16 28-68
1307	PR00290B	Kazal-type serine protease inhibitor signature II	16.63 1.26e-10 39-50
1308	IPB001462G	Hepadnaviral P protein C-terminal domain	17.22 3.38e-09 52-72
1309	IPB001271	Mammalian defensin	19.97 3.42e-21 139-167
1312	IPB002041A	GTP-binding nuclear protein Ran family	11.12 9.36e-12 63-107
1312	PR00449A	Transforming protein P21 ras signature I	12.48 2.57e-16 63-84
1312	PR00449B	Transforming protein P21 ras signature II	14.39 4.81e-09 86-102
1312	PR00449C	Transforming protein P21 ras signature III	15.70 8.26e-12 103-125
1312	PR00449D	Transforming protein P21 ras signature IV	10.27 6.50e-13 167-180
1312	PR00449E	Transforming protein P21 ras signature V	13.39 2.04e-13 201-223
1314	IPB000822	Zinc finger, C2H2 type	14.67 1.69e-18 165-190
1314	IPB000822	Zinc finger, C2H2 type	14.67 1.75e-19 305-330
1314	IPB000822	Zinc finger, C2H2 type	14.67 2.93e-17 277-302
1314	IPB000822	Zinc finger, C2H2 type	14.67 3.08e-18 193-218
1314	IPB000822	Zinc finger, C2H2 type	14.67 6.40e-16 221-246
1314	IPB000822	Zinc finger, C2H2 type	14.67 6.63e-14 333-358
1314	IPB000822	Zinc finger, C2H2 type	14.67 9.31e-18 249-274
1314	IPB001275	DM DNA binding domain	19.17 2.88e-12 321-360
1314	IPB001275	DM DNA binding domain	19.17 3.43e-10 209-248
1314	IPB001275	DM DNA binding domain	19.17 4.16e-10 265-304
1314	IPB001275	DM DNA binding domain	19.17 4.86e-11 237-276
1314	IPB001275	DM DNA binding domain	19.17 5.26e-10 293-332
1314	IPB001275	DM DNA binding domain	19.17 6.66e-11 181-220
1314	PR00048A	C2H2-type zinc finger signature I	9.94 2.23e-10 302-315
1314	PR00048A	C2H2-type zinc finger signature I	9.94 2.29e-13 330-343
1314	PR00048A	C2H2-type zinc finger signature I	9.94 2.93e-13 218-231
1314	PR00048A	C2H2-type zinc finger signature I	9.94 4.86e-13 190-203
1314	PR00048A	C2H2-type zinc finger signature I	9.94 5.26e-11 274-287
1314	PR00048A	C2H2-type zinc finger signature I	9.94 6.14e-13 162-175
1314	PR00048A	C2H2-type zinc finger signature I	9.94 8.07e-13 358-371
1314	PR00048A	C2H2-type zinc finger signature I	9.94 8.88e-09 246-259
1314	PR00048B	C2H2-type zinc finger signature II	5.52 2.29e-10 178-187
1314	PR00048B	C2H2-type zinc finger signature II	5.52 3.57e-10 318-327
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 1.58e-10 78-123
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 1.92e-09 88-133
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 2.06e-10 63-108
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 2.65e-09 28-73
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 2.93e-09 5-50
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 3.07e-12 72-117
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 3.57e-09 82-127
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 4.86e-09 83-128
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 5.06e-10 56-101

Table 3B

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SEQ ID NO:	Database entry ID	Description	Results*
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 5.06e-10 77-122
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 5.10e-11 46-91
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 5.68e-09 36-81
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 5.96e-09 48-93
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 6.30e-11 87-132
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 6.33e-09 25-70
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 6.97e-09 93-138
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 7.48e-10 15-60
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 8.20e-11 101-146
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 8.44e-09 73-118
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 8.81e-09 61-106
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 8.84e-10 33-78
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 9.38e-12 34-79
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 9.82e-09 91-136
1315	IPB000006	Vertebrate metallothionein, family 1	13.41 9.90e-10 102-147
1315	IPB000359B	Cystine-knot domain	19.26 3.48e-10 129-147
1315	IPB000359B	Cystine-knot domain	19.26 6.34e-09 90-108
1315	IPB000437	Prokaryotic membrane lipoprotein lipid attachment site	13.83 7.23e-10 10-21
1315	IPB000437	Prokaryotic membrane lipoprotein lipid attachment site	13.83 9.31e-10 20-31
1315	IPB000726B	Glycoside hydrolase family 19	5.39 5.68e-11 8-18
1315	IPB000726B	Glycoside hydrolase family 19	5.39 7.84e-11 18-28
1315	IPB001007C	von Willebrand factor, type C repeat	20.89 4.27e-09 74-95
1315	IPB001169K	Integrin beta, C-terminus	27.45 1.00e-10 10-52
1315	IPB001169K	Integrin beta, C-terminus	27.45 2.21e-11 81-123
1315	IPB001169K	Integrin beta, C-terminus	27.45 4.04e-09 18-60
1315	IPB001169K	Integrin beta, C-terminus	27.45 4.77e-13 3-45
1315	IPB001169K	Integrin beta, C-terminus	27.45 7.31e-11 13-55
1315	IPB001271	Mammalian defensin	19.97 1.00e-10 12-40
1315	IPB001762A	Disintegrin	23.93 2.24e-09 75-115
1315	IPB001762A	Disintegrin	23.93 2.41e-09 95-135
1315	IPB001762A	Disintegrin	23.93 5.41e-09 114-154
1315	IPB002174A	Furin-like cysteine rich region	30.51 1.79e-11 5-36
1315	IPB002174A	Furin-like cysteine rich region	30.51 1.90e-09 56-87
1315	IPB002174A	Furin-like cysteine rich region	30.51 3.19e-10 12-43
1315	IPB002174A	Furin-like cysteine rich region	30.51 9.16e-12 2-33
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.00e-08 15-48
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.11e-11 122-155
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.67e-12 68-101
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.72e-14 74-107
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.75e-11 49-82
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.00e-12 11-44
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.07e-11 64-97
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.33e-12 54-87
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.85e-17 78-111
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.42e-09 98-131
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.52e-09 79-112
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.00e-15 117-150
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.60e-10 21-54
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.65e-09 102-135
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.93e-11 5-38
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.00e-15 83-116

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.01e-10 63-96
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.13e-09 6-39
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.56e-17 73-106
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.77e-13 16-49
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.24e-10 118-151
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.67e-12 113-146
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.00e-19 112-145
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.16e-10 59-92
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.56e-14 93-126
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.57e-19 88-121
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.65e-09 69-102
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.67e-10 84-117
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.03e-09 89-122
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.71e-09 10-43
1315	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.80e-10 103-136
1315	IPB002494B	Keratin, high sulfur B2 protein	10.58 1.27e-10 141-155
1315	IPB002494B	Keratin, high sulfur B2 protein	10.58 3.92e-09 107-121
1315	IPB002494B	Keratin, high sulfur B2 protein	10.58 4.49e-10 131-145
1315	IPB002494B	Keratin, high sulfur B2 protein	10.58 9.10e-12 102-116
1315	IPB002494B	Keratin, high sulfur B2 protein	10.58 9.10e-12 92-106
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.00e-08 19-62
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.52e-15 86-129
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.59e-09 14-57
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.79e-10 8-51
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.55e-11 62-105
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.66e-13 61-104
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.39e-17 101-144
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.46e-16 110-153
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.80e-10 80-123
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.71e-25 81-124
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.76e-10 67-110
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.11e-10 111-154
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.11e-10 52-95
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.84e-18 76-119
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.42e-10 51-94
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.00e-15 105-148
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.47e-10 85-128
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.62e-15 96-139
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.64e-16 66-109
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.98e-09 95-138
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.07e-24 91-134
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.13e-12 106-149
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.44e-21 71-114
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.45e-11 72-115
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.70e-14 90-133
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.00e-11 46-89
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.30e-14 100-143
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.65e-10 75-118
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.82e-11 77-120
1315	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.83e-09 39-82
1315	IPB003571B	Snake toxin	18.08 1.20e-09 22-45
1315	IPB003854B	Gibberellin regulated protein	19.26 9.51e-10 45-83
1315	PR00858B	Crustacean metallothionein signature II	5.93 3.39e-09 49-67

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1315	PR00858B	Crustacean metallothionein signature II	5.93 7.22e-09 15-33
1315	PR00874C	Fungi-IV metallothionein signature III	4.37 3.75e-09 48-62
1315	PR00876B	Nematode metallothionein signature II	7.66 5.01e-09 89-102
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 1.29e-10 57-102
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 4.12e-09 37-82
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 5.41e-09 52-97
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 5.59e-09 38-83
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 5.68e-09 68-113
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 5.70e-11 47-92
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 5.74e-10 87-132
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 5.87e-09 18-63
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 6.20e-11 88-133
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 6.60e-09 17-62
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 8.35e-09 23-68
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 8.35e-09 78-123
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 8.45e-10 92-137
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 8.70e-11 22-67
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 8.99e-09 33-78
1316	IPB000006	Vertebrate metallothionein, family 1	13.41 9.45e-09 43-88
1316	IPB000359B	Cystine-knot domain	19.26 1.00e-14 90-108
1316	IPB000359B	Cystine-knot domain	19.26 1.56e-09 45-63
1316	IPB000359B	Cystine-knot domain	19.26 2.97e-09 80-98
1316	IPB000359B	Cystine-knot domain	19.26 5.78e-09 120-138
1316	IPB000359B	Cystine-knot domain	19.26 6.25e-12 20-38
1316	IPB000359B	Cystine-knot domain	19.26 8.31e-09 55-73
1316	IPB000359B	Cystine-knot domain	19.26 9.16e-09 25-43
1316	IPB000359B	Cystine-knot domain	19.26 9.16e-09 95-113
1316	IPB000726B	Glycoside hydrolase family 19	5.39 8.46e-09 21-31
1316	IPB000970F	Developmental signaling protein, Wnt-1 family	23.43 5.94e-09 59-107
1316	IPB001271	Mammalian defensin	19.97 1.35e-10 25-53
1316	IPB001271	Mammalian defensin	19.97 1.88e-10 94-122
1316	IPB001271	Mammalian defensin	19.97 2.94e-10 75-103
1316	IPB001271	Mammalian defensin	19.97 4.93e-09 50-78
1316	IPB001271	Mammalian defensin	19.97 4.93e-09 95-123
1316	IPB001271	Mammalian defensin	19.97 5.24e-10 24-52
1316	IPB001271	Mammalian defensin	19.97 5.25e-09 30-58
1316	IPB001271	Mammalian defensin	19.97 5.58e-09 85-113
1316	IPB001271	Mammalian defensin	19.97 7.18e-10 80-108
1316	IPB001271	Mammalian defensin	19.97 7.22e-09 65-93
1316	IPB001271	Mammalian defensin	19.97 7.35e-10 40-68
1316	IPB001271	Mammalian defensin	19.97 8.06e-10 89-117
1316	IPB001271	Mammalian defensin	19.97 8.20e-09 35-63
1316	IPB001271	Mammalian defensin	19.97 8.31e-11 15-43
1316	IPB001271	Mammalian defensin	19.97 8.36e-09 84-112
1316	IPB001271	Mammalian defensin	19.97 8.59e-10 39-67
1316	IPB001271	Mammalian defensin	19.97 8.85e-09 64-92
1316	IPB001271	Mammalian defensin	19.97 8.94e-10 49-77
1316	IPB001271	Mammalian defensin	19.97 9.35e-09 74-102
1316	IPB001271	Mammalian defensin	19.97 9.67e-09 34-62
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.97e-09 94-127
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.23e-18 53-86
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.85e-13 108-141

Table 3B

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SEQ ID NO:	Database entry ID	Description	Results*
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.86e-19 48-81
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.94e-09 49-82
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.33e-12 3-36
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.38e-15 13-46
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.44e-12 18-51
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.67e-12 8-41
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.71e-19 93-126
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.48e-09 54-87
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.68e-10 118-151
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.71e-17 28-61
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.89e-10 24-57
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.97e-09 64-97
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.99e-10 29-62
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.04e-13 43-76
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.10e-17 38-71
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.84e-09 59-92
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.92e-14 88-121
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.63e-15 83-116
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.77e-13 68-101
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.22e-17 73-106
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.58e-09 19-52
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.63e-15 103-136
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.82e-18 23-56
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.07e-16 58-91
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.33e-16 63-96
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.94e-17 98-131
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.03e-09 39-72
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.16e-14 78-111
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.69e-10 89-122
1316	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.76e-14 33-66
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 1.28e-11 22-36
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 2.27e-09 87-101
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 3.69e-10 92-106
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 5.22e-11 77-91
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 5.78e-11 72-86
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.07e-09 52-66
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.20e-11 37-51
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.64e-10 27-41
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.64e-10 97-111
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.91e-10 107-121
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.91e-10 62-76
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 7.08e-09 112-126
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 7.08e-09 67-81
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 9.25e-12 47-61
1316	IPB002494B	Keratin, high sulfur B2 protein	10.58 9.44e-11 117-131
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.00e-08 15-58
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.18e-11 55-98
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.22e-17 101-144
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.36e-11 95-138
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.54e-16 1-44
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.60e-31 41-84
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.94e-26 26-69
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.76e-13 25-68

Table 3B

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SEQ ID NO:	Database entry ID	Description	Results*
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.45e-10 20-63
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.47e-22 56-99
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.09e-12 45-88
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.19e-12 116-159
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.26e-18 21-64
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.47e-24 81-124
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.69e-17 6-49
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.80e-28 76-119
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.84e-10 65-108
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.93e-10 60-103
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.95e-09 100-143
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.01e-13 90-133
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.50e-25 31-74
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.54e-10 35-78
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.54e-10 80-123
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.42e-10 121-164
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.50e-23 46-89
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.52e-21 91-134
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.64e-26 96-139
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.91e-11 85-128
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.04e-22 111-154
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.12e-10 70-113
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.67e-33 16-59
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.75e-28 86-129
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.34e-10 75-118
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.53e-13 50-93
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.70e-20 11-54
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.74e-09 10-53
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.88e-23 36-79
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.88e-28 66-109
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.30e-10 30-73
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.32e-27 51-94
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.38e-23 71-114
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.57e-17 106-149
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.58e-09 105-148
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.60e-25 61-104
1316	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.91e-10 40-83
1316	IPB003888D	FY-rich domain N-terminus	24.70 6.16e-09 100-142
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 1.00e-08 38-83
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 1.18e-09 165-210
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 1.28e-09 85-130
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 1.39e-10 130-175
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 1.46e-09 60-105
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 1.55e-09 70-115
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 2.29e-09 176-221
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 2.35e-10 64-109
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 3.11e-09 69-114
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 3.32e-10 104-149
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 3.94e-09 239-284
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 4.12e-09 125-170
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 5.32e-09 201-246
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 5.59e-09 190-235
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 5.68e-09 175-220

Table 3B

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SEQ ID NO:	Database entry ID	Description	Results*
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 5.68e-09 19-64
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 5.84e-10 210-255
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 5.87e-09 80-125
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 5.94e-10 170-215
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 5.94e-10 200-245
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 6.23e-09 186-231
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 6.88e-09 160-205
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 7.39e-10 225-270
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 7.43e-09 115-160
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 7.43e-09 55-100
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 7.68e-10 24-69
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 7.97e-10 215-260
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 8.35e-09 15-60
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 8.35e-09 45-90
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 8.62e-09 95-140
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 9.13e-10 120-165
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 9.27e-09 205-250
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 9.27e-09 206-251
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 9.45e-09 126-171
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 9.61e-10 34-79
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 9.91e-09 151-196
1317	IPB000006	Vertebrate metallothionein, family 1	13.41 9.91e-09 29-74
1317	IPB000359B	Cystine-knot domain	19.26 1.28e-09 128-146
1317	IPB000359B	Cystine-knot domain	19.26 2.80e-11 163-181
1317	IPB000359B	Cystine-knot domain	19.26 3.53e-09 243-261
1317	IPB000359B	Cystine-knot domain	19.26 4.38e-09 22-40
1317	IPB000359B	Cystine-knot domain	19.26 6.06e-09 248-266
1317	IPB000359B	Cystine-knot domain	19.26 6.34e-09 203-221
1317	IPB000359B	Cystine-knot domain	19.26 6.63e-12 198-216
1317	IPB000359B	Cystine-knot domain	19.26 7.75e-12 62-80
1317	IPB000359B	Cystine-knot domain	19.26 8.88e-09 72-90
1317	IPB000967E	Zinc finger NF-X1 type	21.88 3.73e-09 111-151
1317	IPB000967E	Zinc finger NF-X1 type	21.88 6.46e-09 89-129
1317	IPB001169K	Integrin beta, C-terminus	27.45 5.38e-09 216-258
1317	IPB001271	Mammalian defensin	19.97 1.00e-08 61-89
1317	IPB001271	Mammalian defensin	19.97 1.49e-09 132-160
1317	IPB001271	Mammalian defensin	19.97 1.88e-10 42-70
1317	IPB001271	Mammalian defensin	19.97 2.15e-09 193-221
1317	IPB001271	Mammalian defensin	19.97 2.31e-09 163-191
1317	IPB001271	Mammalian defensin	19.97 2.47e-09 242-270
1317	IPB001271	Mammalian defensin	19.97 2.80e-09 157-185
1317	IPB001271	Mammalian defensin	19.97 3.29e-10 56-84
1317	IPB001271	Mammalian defensin	19.97 4.76e-09 162-190
1317	IPB001271	Mammalian defensin	19.97 5.09e-09 26-54
1317	IPB001271	Mammalian defensin	19.97 5.09e-12 148-176
1317	IPB001271	Mammalian defensin	19.97 5.91e-09 66-94
1317	IPB001271	Mammalian defensin	19.97 6.25e-11 57-85
1317	IPB001271	Mammalian defensin	19.97 6.29e-10 51-79
1317	IPB001271	Mammalian defensin	19.97 6.47e-10 52-80
1317	IPB001271	Mammalian defensin	19.97 6.65e-10 158-186
1317	IPB001271	Mammalian defensin	19.97 7.05e-09 227-255
1317	IPB001271	Mammalian defensin	19.97 7.22e-09 167-195
1317	IPB001271	Mammalian defensin	19.97 7.53e-10 17-45

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1317	IPB001271	Mammalian defensin	19.97 7.71e-10 147-175
1317	IPB001271	Mammalian defensin	19.97 7.87e-09 202-230
1317	IPB001271	Mammalian defensin	19.97 8.20e-09 183-211
1317	IPB001271	Mammalian defensin	19.97 9.18e-09 192-220
1317	IPB001271	Mammalian defensin	19.97 9.35e-09 81-109
1317	IPB001271	Mammalian defensin	19.97 9.67e-09 123-151
1317	IPB001762A	Disintegrin	23.93 4.88e-09 91-131
1317	IPB001762A	Disintegrin	23.93 7.86e-12 99-139
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.00e-14 161-194
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.41e-18 201-234
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.66e-17 166-199
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.72e-10 232-265
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.88e-15 196-229
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.16e-16 50-83
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.35e-09 5-38
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.44e-12 80-113
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.44e-14 106-139
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.67e-16 131-164
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.67e-16 146-179
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.84e-10 251-284
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.12e-17 40-73
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.42e-09 97-130
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.42e-13 15-48
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.43e-19 171-204
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.43e-19 206-239
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.57e-16 25-58
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.81e-09 41-74
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.86e-19 226-259
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.88e-15 176-209
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.00e-09 81-114
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.23e-13 211-244
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.36e-14 45-78
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.44e-17 181-214
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.71e-17 30-63
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.87e-09 112-145
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.89e-12 111-144
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.00e-19 191-224
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.27e-13 96-129
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.35e-09 177-210
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.40e-10 26-59
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.50e-15 101-134
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.71e-11 151-184
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.73e-13 60-93
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.14e-16 35-68
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.28e-14 75-108
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.61e-09 237-270
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.66e-16 136-169
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.66e-16 65-98
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.66e-16 70-103
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.71e-09 36-69
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.73e-18 156-189
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.79e-11 221-254
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.00e-11 20-53

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.11e-11 126-159
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.17e-16 121-154
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.22e-17 216-249
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.44e-12 186-219
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.58e-09 76-109
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.77e-09 182-215
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.97e-09 142-175
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.00e-12 236-269
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.07e-16 55-88
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.47e-10 246-279
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.67e-10 6-39
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.93e-11 141-174
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.13e-15 231-264
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.33e-12 241-274
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.81e-09 207-240
1317	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.90e-09 85-118
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 1.00e-09 160-174
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 1.45e-12 190-204
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 1.45e-12 225-239
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 1.63e-09 89-103
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 2.75e-10 125-139
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 3.11e-11 54-68
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 3.81e-11 120-134
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 5.64e-11 49-63
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 5.69e-09 180-194
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 5.69e-09 215-229
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 5.84e-10 19-33
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 5.92e-11 155-169
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.07e-09 69-83
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.58e-09 185-199
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.58e-09 220-234
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.96e-09 59-73
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 7.08e-09 150-164
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 7.08e-09 195-209
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 7.97e-09 79-93
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 8.52e-10 170-184
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 8.52e-10 205-219
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 9.25e-12 64-78
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 9.33e-10 130-144
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 9.37e-09 94-108
1317	IPB002494B	Keratin, high sulfur B2 protein	10.58 9.62e-09 240-254
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.12e-21 154-197
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.23e-18 13-56
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.35e-10 89-132
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.38e-12 22-65
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.59e-09 72-115
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.71e-20 224-267
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.73e-11 27-70
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.91e-11 37-80
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.11e-22 209-252
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.13e-12 84-127
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.22e-10 123-166
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.22e-12 168-211

Table 3B

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SEQ ID NO:	Database entry ID	Description	Results*
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.29e-29 184-227
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.31e-10 42-85
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.45e-15 99-142
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.48e-19 33-76
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.50e-14 234-277
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.55e-15 98-141
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.57e-29 58-101
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.60e-09 47-90
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.64e-11 143-186
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.00e-23 179-222
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.09e-11 133-176
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.36e-09 223-266
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.38e-23 204-247
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.44e-09 238-281
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.86e-09 218-261
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.90e-32 194-237
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.97e-10 12-55
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.06e-10 188-231
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.18e-11 178-221
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.36e-11 67-110
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.36e-21 199-242
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.49e-18 144-187
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.52e-28 43-86
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.55e-27 229-272
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.67e-10 158-201
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.84e-12 198-241
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.04e-09 103-146
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.10e-25 169-212
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.19e-10 153-196
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.50e-14 94-137
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.50e-18 83-126
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.50e-25 68-111
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.90e-14 244-287
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.16e-12 213-256
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.16e-21 214-257
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.19e-32 159-202
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.25e-23 174-217
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.35e-19 239-282
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.57e-16 78-121
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.74e-18 129-172
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.91e-12 62-105
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.96e-17 119-162
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.00e-11 173-216
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.00e-12 128-171
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.12e-10 208-251
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.19e-28 124-167
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.21e-16 3-46
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.30e-18 73-116
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.43e-24 134-177
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.50e-23 53-96
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.55e-10 32-75
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.64e-11 193-236
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.73e-10 148-191

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.75e-20 114-157
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.88e-23 189-232
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.99e-20 109-152
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.03e-12 163-206
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.05e-31 149-192
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.15e-22 28-71
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.22e-12 8-51
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.25e-23 164-207
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.32e-21 23-66
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.81e-25 18-61
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.91e-09 77-120
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.92e-17 249-292
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.02e-17 88-131
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.04e-10 57-100
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.24e-09 19-62
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.32e-13 203-246
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.41e-20 63-106
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.43e-19 139-182
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.51e-22 38-81
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.73e-26 48-91
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.74e-10 108-151
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.82e-11 52-95
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.86e-28 219-262
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.89e-16 93-136
1317	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.90e-14 104-147
1317	PR00876B	Nematode metallothionein signature II	7.66 9.76e-09 113-126
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 1.00e-08 42-87
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 2.10e-09 125-170
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 2.74e-09 34-79
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 3.59e-12 124-169
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 4.21e-12 119-164
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 4.58e-09 32-77
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 4.67e-09 94-139
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 5.04e-09 88-133
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 5.13e-09 101-146
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 5.16e-10 100-145
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 5.20e-11 109-154
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 5.40e-11 120-165
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 5.65e-10 114-159
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 5.68e-09 110-155
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 5.78e-09 104-149
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 5.96e-09 55-100
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 6.03e-10 98-143
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 6.50e-11 35-80
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 6.59e-12 115-160
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 6.97e-09 111-156
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 7.61e-09 43-88
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 9.23e-10 83-128
1318	IPB0000006	Vertebrate metallothionein, family 1	13.41 9.67e-13 93-138
1318	IPB000254	Cellulose-binding domain, fungal type	18.11 6.86e-09 94-124
1318	IPB000359B	Cystine-knot domain	19.26 3.25e-12 147-165
1318	IPB000359B	Cystine-knot domain	19.26 5.29e-13 127-145
1318	IPB000726A	Glycoside hydrolase family 19	14.41 9.88e-09 3-29

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1318	IPB000726B	Glycoside hydrolase family 19	5.39 3.40e-10 16-26
1318	IPB000726B	Glycoside hydrolase family 19	5.39 3.40e-10 9-19
1318	IPB001007C	von Willebrand factor, type C repeat	20.89 4.27e-09 111-132
1318	IPB001169K	Integrin beta, C-terminus	27.45 3.07e-09 118-160
1318	IPB001169K	Integrin beta, C-terminus	27.45 5.62e-09 25-67
1318	IPB001169K	Integrin beta, C-terminus	27.45 8.91e-09 35-77
1318	IPB001271	Mammalian defensin	19.97 5.91e-09 142-170
1318	IPB001271	Mammalian defensin	19.97 6.89e-09 107-135
1318	IPB001271	Mammalian defensin	19.97 8.41e-10 21-49
1318	IPB001762A	Disintegrin	23.93 3.03e-13 112-152
1318	IPB001762A	Disintegrin	23.93 4.18e-09 113-153
1318	IPB001762A	Disintegrin	23.93 5.60e-10 103-143
1318	IPB001762A	Disintegrin	23.93 5.60e-10 123-163
1318	IPB002174A	Furin-like cysteine rich region	30.51 1.97e-10 83-114
1318	IPB002174A	Furin-like cysteine rich region	30.51 3.92e-10 93-124
1318	IPB002174A	Furin-like cysteine rich region	30.51 8.20e-09 73-104
1318	IPB002174A	Furin-like cysteine rich region	30.51 8.88e-09 17-48
1318	IPB002174A	Furin-like cysteine rich region	30.51 9.27e-10 3-34
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.11e-11 101-134
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.13e-17 130-163
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.31e-10 116-149
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.78e-12 105-138
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.00e-12 25-58
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.16e-09 31-64
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.63e-15 140-173
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.32e-18 115-148
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.44e-16 135-168
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.21e-16 120-153
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.48e-10 100-133
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.04e-13 91-124
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.81e-10 30-63
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.32e-09 106-139
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.67e-12 14-47
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.89e-12 20-53
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.03e-10 96-129
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.65e-10 121-154
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.35e-09 21-54
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.88e-15 111-144
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.03e-09 26-59
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.22e-12 86-119
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.25e-11 24-57
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.57e-19 110-143
1318	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.73e-18 125-158
1318	IPB002494B	Keratin, high sulfur B2 protein	10.58 1.51e-09 124-138
1318	IPB002494B	Keratin, high sulfur B2 protein	10.58 2.27e-09 159-173
1318	IPB002494B	Keratin, high sulfur B2 protein	10.58 3.55e-12 139-153
1318	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.70e-12 129-143
1318	IPB002494B	Keratin, high sulfur B2 protein	10.58 8.45e-11 149-163
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.27e-11 114-157
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.27e-11 99-142
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.41e-27 128-171
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.70e-10 104-147
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.08e-13 98-141

Table 3B

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SEQ ID NO:	Database entry ID	Description	Results*
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.48e-18 113-156
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.88e-10 107-150
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.09e-11 112-155
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.70e-09 102-145
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.84e-21 108-151
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.10e-19 123-166
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.55e-11 17-60
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.77e-17 103-146
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.82e-11 109-152
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.87e-13 23-66
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.81e-09 94-137
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.84e-12 122-165
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.40e-09 48-91
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.57e-29 118-161
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.69e-10 88-131
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.69e-12 117-160
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.33e-09 93-136
1318	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.71e-13 127-170
1318	IPB003571B	Snake toxin	18.08 4.72e-09 32-55
1318	PR00874C	Fungi-IV metallothionein signature III	4.37 9.74e-10 95-109
1318	PR00876B	Nematode metallothionein signature II	7.66 2.27e-10 107-120
1319	IPB000822	Zinc finger, C2H2 type	14.67 3.08e-18 175-200
1319	IPB000822	Zinc finger, C2H2 type	14.67 4.75e-19 147-172
1319	IPB000822	Zinc finger, C2H2 type	14.67 4.94e-14 119-144
1319	IPB000822	Zinc finger, C2H2 type	14.67 7.92e-18 63-88
1319	IPB000822	Zinc finger, C2H2 type	14.67 8.36e-21 203-228
1319	IPB000822	Zinc finger, C2H2 type	14.67 8.36e-21 91-116
1319	IPB000822	Zinc finger, C2H2 type	14.67 9.31e-18 35-60
1319	IPB001222	TFIIS zinc ribbon domain	24.63 6.70e-09 175-211
1319	IPB001275	DM DNA binding domain	19.17 3.43e-13 79-118
1319	IPB001275	DM DNA binding domain	19.17 4.77e-10 163-202
1319	IPB001275	DM DNA binding domain	19.17 6.91e-11 51-90
1319	IPB001275	DM DNA binding domain	19.17 7.20e-10 107-146
1319	IPB001275	DM DNA binding domain	19.17 9.09e-09 23-62
1319	IPB001275	DM DNA binding domain	19.17 9.10e-14 135-174
1319	IPB001275	DM DNA binding domain	19.17 9.29e-13 191-230
1319	IPB002867C	Cysteine-rich domain (C6HC)	19.46 8.34e-09 32-49
1319	PR00048A	C2H2-type zinc finger signature I	9.94 2.23e-10 200-213
1319	PR00048A	C2H2-type zinc finger signature I	9.94 3.84e-11 60-73
1319	PR00048A	C2H2-type zinc finger signature I	9.94 4.38e-09 88-101
1319	PR00048A	C2H2-type zinc finger signature I	9.94 5.50e-10 32-45
1319	PR00048A	C2H2-type zinc finger signature I	9.94 8.77e-10 172-185
1319	PR00048A	C2H2-type zinc finger signature I	9.94 9.18e-10 144-157
1319	PR00048B	C2H2-type zinc finger signature II	5.52 1.00e-08 132-141
1319	PR00048B	C2H2-type zinc finger signature II	5.52 2.50e-09 48-57
1319	PR00048B	C2H2-type zinc finger signature II	5.52 3.57e-10 160-169
1319	PR00048B	C2H2-type zinc finger signature II	5.52 4.00e-11 104-113
1319	PR00048B	C2H2-type zinc finger signature II	5.52 5.50e-09 76-85
1319	PR00048B	C2H2-type zinc finger signature II	5.52 6.14e-10 188-197
1319	PR00048B	C2H2-type zinc finger signature II	5.52 7.75e-11 216-225
1320	IPB002041A	GTP-binding nuclear protein Ran family	11.12 9.17e-10 4-48
1320	PR00449A	Transforming protein P21 ras signature I	12.48 1.29e-14 4-25
1321	IPB000006	Vertebrate metallothionein, family 1	13.41 6.00e-11 71-116

Table 3B

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SEQ ID NO:	Database entry ID	Description	Results*
1321	IPB000006	Vertebrate metallothionein, family 1	13.41 9.72e-09 146-191
1321	IPB000726B	Glycoside hydrolase family 19	5.39 2.54e-09 66-76
1321	IPB000967E	Zinc finger NF-X1 type	21.88 1.24e-09 95-135
1321	IPB001169K	Integrin beta, C-terminus	27.45 5.38e-09 56-98
1321	IPB001762A	Disintegrin	23.93 9.29e-09 69-109
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.56e-12 161-194
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.06e-09 146-179
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 2.94e-09 103-136
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.00e-14 81-114
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 4.19e-09 72-105
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.26e-09 67-100
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.38e-13 156-189
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 5.56e-14 71-104
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.32e-09 166-199
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 6.56e-12 123-156
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.34e-10 124-157
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.39e-09 82-115
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.48e-09 151-184
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.58e-09 57-90
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.60e-14 118-151
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.97e-09 86-119
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.33e-12 113-146
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.35e-09 62-95
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.97e-16 76-109
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.13e-09 147-180
1321	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.14e-11 66-99
1321	IPB002494B	Keratin, high sulfur B2 protein	10.58 1.13e-09 70-84
1321	IPB002494B	Keratin, high sulfur B2 protein	10.58 3.53e-11 122-136
1321	IPB002494B	Keratin, high sulfur B2 protein	10.58 4.17e-09 142-156
1321	IPB002494B	Keratin, high sulfur B2 protein	10.58 4.17e-09 22-36
1321	IPB002494B	Keratin, high sulfur B2 protein	10.58 5.56e-09 137-151
1321	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.58e-09 80-94
1321	IPB002494B	Keratin, high sulfur B2 protein	10.58 6.78e-10 95-109
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.50e-14 21-64
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.59e-09 70-113
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 1.96e-10 6-49
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.01e-09 36-79
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.20e-21 74-117
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.27e-13 164-207
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.55e-11 26-69
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.70e-14 159-202
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.86e-13 149-192
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.10e-09 131-174
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.10e-09 75-118
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 3.30e-14 126-169
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.19e-12 84-127
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 4.36e-17 116-159
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.36e-11 144-187
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.61e-16 79-122
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 5.79e-09 145-188
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.06e-12 111-154
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.53e-12 11-54
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 6.91e-12 89-132

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.10e-15 64-107
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.31e-15 121-164
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.82e-11 169-212
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.85e-13 59-102
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 7.99e-10 139-182
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 8.76e-18 154-197
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.07e-09 27-70
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.44e-12 31-74
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.66e-18 69-112
1321	IPB002494C	Keratin, high sulfur B2 protein	14.46 9.73e-11 106-149
1321	IPB002919A	Trypsin Inhibitor-like cysteine rich domain	15.56 6.57e-09 24-36
1327	IPB000118B	Granulin	7.94 1.30e-10 29-67
1327	IPB000118G	Granulin	12.18 8.85e-09 18-66
1327	IPB000203A	GPS domain	18.40 4.65e-09 44-74
1327	IPB000203A	GPS domain	18.40 5.57e-09 86-116
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 1.64e-09 58-103
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 2.70e-11 54-99
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 3.39e-09 70-115
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 3.66e-09 75-120
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 4.87e-10 51-96
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 5.59e-09 57-102
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 6.00e-11 50-95
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 6.42e-09 65-110
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 7.98e-09 40-85
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 8.07e-09 55-100
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 8.48e-13 47-92
1329	IPB000006	Vertebrate metallothionein, family 1	13.41 8.94e-10 74-119
1329	IPB000254	Cellulose-binding domain, fungal type	18.11 7.00e-09 43-73
1329	IPB000564A	2Fe-2S Ferredoxin	17.31 7.80e-09 1-19
1329	IPB000817A	Prion protein	8.34 1.85e-09 13-55
1329	IPB000817A	Prion protein	8.34 4.79e-09 9-51
1329	IPB000817A	Prion protein	8.34 6.87e-09 12-54
1329	IPB000817A	Prion protein	8.34 8.64e-11 6-48
1329	IPB000817A	Prion protein	8.34 9.01e-10 10-52
1329	IPB000967D	Zinc finger NF-X1 type	10.42 7.77e-09 75-110
1329	IPB001169K	Integrin beta, C-terminus	27.45 3.19e-09 57-99
1329	IPB001169K	Integrin beta, C-terminus	27.45 8.05e-09 72-114
1329	IPB001169K	Integrin beta, C-terminus	27.45 9.15e-09 16-58
1329	IPB001271	Mammalian defensin	19.97 3.29e-10 66-94
1329	IPB001271	Mammalian defensin	19.97 4.44e-09 73-101
1329	IPB001271	Mammalian defensin	19.97 5.42e-09 82-110
1329	IPB001271	Mammalian defensin	19.97 7.35e-10 44-72
1329	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 2.10e-09 4-56
1329	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 2.80e-09 1-53
1329	IPB002174A	Furin-like cysteine rich region	30.51 2.58e-09 51-82
1329	IPB002174A	Furin-like cysteine rich region	30.51 4.38e-09 34-65
1329	IPB002174A	Furin-like cysteine rich region	30.51 4.97e-11 2-33
1329	IPB002174A	Furin-like cysteine rich region	30.51 5.28e-09 6-37
1329	IPB002174A	Furin-like cysteine rich region	30.51 6.35e-10 26-57
1329	IPB002174A	Furin-like cysteine rich region	30.51 7.62e-11 30-61
1329	IPB002174A	Furin-like cysteine rich region	30.51 9.27e-10 18-49

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SEQ ID NO:	Database entry ID	Description	Results*
1329	IPB002174A	Furin-like cysteine rich region	30.51 9.27e-10 22-53
1329	IPB002221B	WAP-type (Whey Acidic Protein) four-disulfide core domain	17.12 1.00e-08 63-84
1329	IPB002494A	Keratin, high sulfur B2 protein	12.44 1.39e-09 44-77
1329	IPB002494A	Keratin, high sulfur B2 protein	12.44 3.23e-09 34-67
1329	IPB002494A	Keratin, high sulfur B2 protein	12.44 7.75e-10 85-118
1329	IPB002494A	Keratin, high sulfur B2 protein	12.44 8.67e-10 47-80
1329	IPB002494A	Keratin, high sulfur B2 protein	12.44 9.03e-09 40-73
1329	IPB002494C	Keratin, high sulfur B2 protein	14.46 2.31e-10 60-103
1329	IPB002551P	Coronavirus S1 glycoprotein	13.91 7.68e-09 79-120
1329	IPB002867D	Cysteine-rich domain (C6HC)	24.88 6.49e-09 53-84
1329	IPB002919A	Trypsin Inhibitor-like cysteine rich domain	15.56 3.57e-09 67-79
1329	PR00858B	Crustacean metallothionein signature II	5.93 1.48e-09 55-73
1329	PR00872A	Diptera (Drosophila) metallothionein signature I	5.17 7.41e-09 99-111
1329	PR01117A	CLC-6 chloride channel signature I	7.79 9.47e-09 66-78
1329	PR01131B	Connexin36 (Cx36) signature II	3.45 5.12e-09 42-54
1329	PR01228C	Eggshell protein signature III	5.69 1.22e-10 17-32
1329	PR01228C	Eggshell protein signature III	5.69 1.22e-10 21-36
1329	PR01228C	Eggshell protein signature III	5.69 1.22e-10 25-40
1329	PR01228C	Eggshell protein signature III	5.69 1.22e-10 29-44
1329	PR01228C	Eggshell protein signature III	5.69 1.22e-10 33-48
1329	PR01228C	Eggshell protein signature III	5.69 1.22e-10 37-52
1329	PR01228C	Eggshell protein signature III	5.69 2.34e-09 41-56
1329	PR01228C	Eggshell protein signature III	5.69 5.86e-09 18-33
1329	PR01228C	Eggshell protein signature III	5.69 5.86e-09 22-37
1329	PR01228C	Eggshell protein signature III	5.69 5.86e-09 26-41
1329	PR01228C	Eggshell protein signature III	5.69 5.86e-09 30-45
1329	PR01228C	Eggshell protein signature III	5.69 5.86e-09 34-49
1329	PR01228C	Eggshell protein signature III	5.69 5.86e-09 38-53
1329	PR01228C	Eggshell protein signature III	5.69 6.48e-09 13-28
1330	IPB000221	Protamine P1	5.48 1.00e-08 76-102
1330	IPB000221	Protamine P1	5.48 1.00e-09 83-109
1330	IPB000221	Protamine P1	5.48 1.46e-09 65-91
1330	IPB000221	Protamine P1	5.48 2.19e-11 103-129
1330	IPB000221	Protamine P1	5.48 2.59e-11 64-90
1330	IPB000221	Protamine P1	5.48 2.73e-10 118-144
1330	IPB000221	Protamine P1	5.48 2.97e-12 74-100
1330	IPB000221	Protamine P1	5.48 3.31e-09 109-135
1330	IPB000221	Protamine P1	5.48 3.31e-09 122-148
1330	IPB000221	Protamine P1	5.48 3.91e-11 78-104
1330	IPB000221	Protamine P1	5.48 4.70e-10 62-88
1330	IPB000221	Protamine P1	5.48 4.70e-10 94-120
1330	IPB000221	Protamine P1	5.48 5.15e-09 107-133
1330	IPB000221	Protamine P1	5.48 5.27e-09 52-78
1330	IPB000221	Protamine P1	5.48 6.16e-11 92-118
1330	IPB000221	Protamine P1	5.48 6.19e-09 116-142
1330	IPB000221	Protamine P1	5.48 6.43e-11 99-125
1330	IPB000221	Protamine P1	5.48 6.88e-09 111-137
1330	IPB000221	Protamine P1	5.48 6.88e-09 97-123
1330	IPB000221	Protamine P1	5.48 7.62e-11 60-86
1330	IPB000221	Protamine P1	5.48 8.89e-10 101-127
1330	IPB000221	Protamine P1	5.48 9.30e-12 63-89

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SEQ ID NO:	Database entry ID	Description	Results*
1330	IPB000271	Ribosomal protein L34	15.87 9.78e-09 111-148
1330	IPB000492B	Protamine 2 (PRM2)	5.26 3.84e-09 75-109
1330	IPB000492B	Protamine 2 (PRM2)	5.26 5.88e-11 98-132
1330	IPB000492B	Protamine 2 (PRM2)	5.26 6.38e-09 94-128
1330	IPB000492B	Protamine 2 (PRM2)	5.26 6.67e-09 107-141
1330	IPB000492B	Protamine 2 (PRM2)	5.26 6.97e-10 103-137
1330	IPB000492B	Protamine 2 (PRM2)	5.26 7.75e-09 77-111
1330	IPB000492B	Protamine 2 (PRM2)	5.26 8.12e-10 106-140
1330	IPB000492B	Protamine 2 (PRM2)	5.26 8.34e-09 65-99
1330	IPB000492B	Protamine 2 (PRM2)	5.26 8.53e-10 105-139
1330	IPB000492B	Protamine 2 (PRM2)	5.26 9.06e-10 78-112
1330	IPB000492B	Protamine 2 (PRM2)	5.26 9.35e-11 102-136
1330	IPB000492B	Protamine 2 (PRM2)	5.26 9.35e-11 79-113
1330	IPB000492B	Protamine 2 (PRM2)	5.26 9.69e-10 100-134
1330	IPB000492B	Protamine 2 (PRM2)	5.26 9.90e-09 111-145
1330	IPB003134F	Repeat in HS1/Cortactin	15.66 7.21e-09 183-231
1330	PR00055C	HIV TAT domain signature III	9.12 5.92e-09 16-32
1331	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 2.80e-10 54-91
1332	IPB002223	Pancreatic trypsin inhibitor (Kunitz) family	17.66 2.61e-23 92-126
1332	PR00759A	Basic protease (Kunitz-type) inhibitor family signature I	14.67 5.71e-10 73-87
1332	PR00759B	Basic protease (Kunitz-type) inhibitor family signature II	12.35 1.28e-10 101-111
1332	PR00759C	Basic protease (Kunitz-type) inhibitor family signature III	12.43 2.24e-11 111-126
1333	IPB000822	Zinc finger, C2H2 type	14.67 1.75e-19 201-226
1333	IPB000822	Zinc finger, C2H2 type	14.67 1.75e-20 341-366
1333	IPB000822	Zinc finger, C2H2 type	14.67 2.13e-15 369-394
1333	IPB000822	Zinc finger, C2H2 type	14.67 5.50e-20 229-254
1333	IPB000822	Zinc finger, C2H2 type	14.67 5.91e-21 285-310
1333	IPB000822	Zinc finger, C2H2 type	14.67 7.00e-20 313-338
1333	IPB000822	Zinc finger, C2H2 type	14.67 9.10e-22 257-282
1333	IPB001275	DM DNA binding domain	19.17 1.29e-13 245-284
1333	IPB001275	DM DNA binding domain	19.17 2.34e-12 329-368
1333	IPB001275	DM DNA binding domain	19.17 2.95e-10 217-256
1333	IPB001275	DM DNA binding domain	19.17 3.51e-09 357-396
1333	IPB001275	DM DNA binding domain	19.17 7.00e-13 273-312
1333	IPB001275	DM DNA binding domain	19.17 7.15e-14 301-340
1333	IPB001909	KRAB box	17.37 9.10e-31 8-42
1333	PR00048A	C2H2-type zinc finger signature I	9.94 1.00e-13 198-211
1333	PR00048A	C2H2-type zinc finger signature I	9.94 1.64e-13 254-267
1333	PR00048A	C2H2-type zinc finger signature I	9.94 1.64e-13 282-295
1333	PR00048A	C2H2-type zinc finger signature I	9.94 6.21e-11 226-239
1333	PR00048A	C2H2-type zinc finger signature I	9.94 6.79e-13 366-379
1333	PR00048A	C2H2-type zinc finger signature I	9.94 9.36e-13 310-323
1333	PR00048A	C2H2-type zinc finger signature I	9.94 9.53e-11 338-351
1333	PR00048B	C2H2-type zinc finger signature II	5.52 1.00e-09 270-279
1333	PR00048B	C2H2-type zinc finger signature II	5.52 2.29e-10 326-335
1333	PR00048B	C2H2-type zinc finger signature II	5.52 2.50e-11 242-251
1333	PR00048B	C2H2-type zinc finger signature II	5.52 7.00e-09 298-307
1333	PR00048B	C2H2-type zinc finger signature II	5.52 7.00e-12 354-363
1333	PR00048B	C2H2-type zinc finger signature II	5.52 7.50e-09 214-223

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SEQ ID NO:	Database entry ID	Description	Results*
1336	PR00806B	Vinculin signature II	4.27 9.04e-09 333-346
1336	PR00806B	Vinculin signature II	4.27 9.64e-09 332-345
1336	PR01217G	Proline rich extensin signature VII	4.02 7.47e-09 399-424
1337	PR00806B	Vinculin signature II	4.27 9.04e-09 333-346
1337	PR00806B	Vinculin signature II	4.27 9.64e-09 332-345
1337	PR01217G	Proline rich extensin signature VII	4.02 7.47e-09 399-424
1338	IPB001526A	Ly-6/u-PAR domain	13.24 8.33e-09 7-22
1338	PR01226A	Expansin signature I	5.84 6.11e-09 259-273
1339	IPB000729D	PMP-22/EMP/MP20 family	18.96 7.30e-10 182-209
1340	IPB000729D	PMP-22/EMP/MP20 family	18.96 7.30e-10 173-200
1341	IPB003397B	Mitochondrial import inner membrane translocase subunit Tim17	21.18 9.79e-10 60-105
1343	IPB000353B	Class II histocompatibility antigen, beta chain, beta-1 domain	19.16 4.94e-16 187-236
1343	IPB001003B	MHC Class II, alpha chain, alpha-1 domain	14.72 9.90e-10 195-238
1343	IPB003006A	Immunoglobulin and major histocompatibility complex domain	17.51 8.50e-16 208-230
1344	IPB002499N	Major Vault Protein repeat	12.73 9.47e-09 220-273
1345	PR00462B	Fungal lignin peroxidase family signature II	14.83 4.74e-09 34-52
1347	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 3.77e-09 202-239
1347	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 8.83e-11 306-343
1347	PR01236A	Tumour necrosis factor beta (lymphotoxin-alpha) signature I	4.92 5.60e-09 3-19
1348	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 1.36e-10 403-440
1350	PR01218B	Pistil-specific extensin-like signature II	8.47 4.88e-09 115-138
1353	PR00019A	Leucine-rich repeat signature I	11.72 7.33e-10 193-206
1356	IPB002896F	Herpesvirus glycoprotein D	21.08 9.22e-09 327-362
1356	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 5.15e-09 276-313
1357	IPB002159A	CD36 family	36.08 5.26e-39 258-311
1357	IPB002159B	CD36 family	29.25 5.13e-34 334-379
1359	IPB003006A	Immunoglobulin and major histocompatibility complex domain	17.51 1.00e-10 160-182
1359	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 6.09e-11 206-243
1363	PR01432K	Rabaptin signature XI	2.19 8.43e-09 873-895
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 1.00e-15 200-237
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 1.20e-10 167-204
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 1.25e-16 191-228
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 2.00e-13 203-240
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 2.20e-20 179-216
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 2.80e-18 176-213
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 4.29e-19 182-219
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 6.58e-10 209-246
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 7.15e-09 164-201
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 7.85e-16 173-210
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 8.20e-20 185-222
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 8.99e-11 206-243
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 9.03e-15 197-234
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 9.11e-13 170-207
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 9.37e-16 194-231

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SEQ ID NO:	Database entry ID	Description	Results*
1366	IPB000885A	Fibrillar collagen C-terminal domain	11.46 9.71e-19 188-225
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 1.12e-19 174-227
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 2.73e-20 186-239
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 3.59e-17 171-224
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 4.58e-16 189-242
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 5.11e-10 153-206
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 5.31e-12 159-212
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 5.77e-16 192-245
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 5.98e-15 162-215
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 6.06e-14 165-218
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 6.18e-20 177-230
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 6.46e-14 195-248
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 6.66e-10 201-254
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 6.87e-13 198-251
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 7.36e-19 168-221
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 7.55e-13 156-209
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 8.78e-12 150-203
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 9.16e-24 180-233
1366	IPB000885B	Fibrillar collagen C-terminal domain	19.15 9.60e-22 183-236
1366	IPB001073A	Complement C1q protein	22.14 1.00e-13 202-236
1366	IPB001073A	Complement C1q protein	22.14 1.46e-16 193-227
1366	IPB001073A	Complement C1q protein	22.14 2.76e-15 196-230
1366	IPB001073A	Complement C1q protein	22.14 3.77e-16 190-224
1366	IPB001073A	Complement C1q protein	22.14 3.90e-10 208-242
1366	IPB001073A	Complement C1q protein	22.14 4.69e-16 175-209
1366	IPB001073A	Complement C1q protein	22.14 5.83e-15 178-212
1366	IPB001073A	Complement C1q protein	22.14 6.18e-19 184-218
1366	IPB001073A	Complement C1q protein	22.14 7.51e-13 181-215
1366	IPB001073A	Complement C1q protein	22.14 8.02e-15 205-239
1366	IPB001073A	Complement C1q protein	22.14 8.40e-14 199-233
1366	IPB001073A	Complement C1q protein	22.14 8.78e-10 172-206
1366	IPB001073A	Complement C1q protein	22.14 8.85e-13 187-221
1366	IPB001073B	Complement C1q protein	20.88 7.26e-29 281-315
1366	IPB001073C	Complement C1q protein	13.07 1.87e-14 349-368
1366	IPB001073D	Complement C1q protein	7.60 8.20e-13 383-392
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 1.44e-18 169-221
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 1.52e-23 181-233
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 2.08e-14 160-212
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 3.00e-18 166-218
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 3.20e-16 202-254
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 3.25e-12 157-209
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 3.72e-13 196-248
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 3.93e-17 193-245
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 3.97e-12 199-251
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 4.08e-21 175-227

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SEQ ID NO:	Database entry ID	Description	Results*
		4 procollagen	
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 4.45e-16 190-242
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 4.74e-19 184-236
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 6.01e-22 172-224
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 6.24e-09 154-206
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 6.40e-22 178-230
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 6.54e-11 148-200
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 6.86e-17 187-239
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 6.97e-16 163-215
1366	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 8.47e-12 151-203
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 1.57e-11 209-229
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 2.34e-09 182-202
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 2.82e-09 188-208
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 3.55e-09 179-199
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 4.00e-11 206-226
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 4.47e-10 191-211
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 5.01e-09 203-223
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 5.24e-10 194-214
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 7.30e-10 200-220
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 7.57e-11 197-217
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 7.93e-09 176-196
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 8.42e-09 185-205
1366	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 8.66e-09 212-232
1366	PR00007A	Complement C1Q domain signature I	20.64 6.54e-20 274-300
1366	PR00007B	Complement C1Q domain signature II	15.63 3.13e-14 301-320
1366	PR00007C	Complement C1Q domain signature III	16.13 2.62e-15 349-370
1366	PR00007D	Complement C1Q domain signature IV	9.66 1.95e-12 381-391
1367	IPB001427A	Pancreatic ribonuclease family	12.97 1.41e-10 31-40
1367	IPB001427B	Pancreatic ribonuclease family	31.44 4.30e-29 45-95
1367	IPB001427C	Pancreatic ribonuclease family	24.33 8.07e-20 83-113
1367	PR00794A	Pancreatic ribonuclease family signature I	15.68 1.00e-18 46-65
1367	PR00794B	Pancreatic ribonuclease family signature II	17.91 7.55e-16 66-85

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1367	PR00794D	Pancreatic ribonuclease family signature IV	19.74 6.40e-20 94-116
1368	IPB000171A	Bacterial-type phytoene dehydrogenase	19.28 9.72e-11 57-87
1368	IPB000927A	D-amino acid oxidase	8.56 7.91e-09 55-67
1368	IPB002135A	3-hydroxyacyl-CoA dehydrogenase	20.39 2.50e-10 58-83
1369	IPB000171A	Bacterial-type phytoene dehydrogenase	19.28 9.72e-11 57-87
1369	IPB000927A	D-amino acid oxidase	8.56 7.91e-09 55-67
1369	IPB002135A	3-hydroxyacyl-CoA dehydrogenase	20.39 2.50e-10 58-83
1371	PR00762A	Chloride channel signature I	14.76 7.95e-19 108-125
1371	PR00762B	Chloride channel signature II	11.84 2.97e-16 139-158
1371	PR00762C	Chloride channel signature III	9.42 3.57e-20 203-222
1371	PR00762D	Chloride channel signature IV	11.34 4.54e-19 440-460
1371	PR00762E	Chloride channel signature V	11.24 8.45e-16 475-491
1371	PR00762F	Chloride channel signature VI	15.29 4.18e-15 493-512
1371	PR00762G	Chloride channel signature VII	13.53 7.19e-12 531-545
1371	PR01117A	CLC-6 chloride channel signature I	7.79 1.09e-19 2-14
1371	PR01117C	CLC-6 chloride channel signature III	9.38 1.19e-17 54-66
1371	PR01117D	CLC-6 chloride channel signature IV	6.15 1.10e-13 159-168
1371	PR01117E	CLC-6 chloride channel signature V	7.29 1.10e-13 170-179
1372	IPB000276A	Rhodopsin-like GPCR superfamily	11.56 1.69e-13 159-170
1372	PR00245A	Olfactory receptor signature I	10.98 2.50e-13 133-144
1372	PR00245B	Olfactory receptor signature II	13.73 5.70e-12 170-182
1372	PR00534A	Melanocortin receptor family signature I	12.77 8.04e-09 92-104
1372	PR00642C	EDG-1 sphingosine 1-phosphate receptor signature III	13.87 4.43e-09 89-101
1374	IPB000109A	PTR peptide transporters (PTR2)	10.85 3.79e-15 44-62
1374	IPB000109B	PTR peptide transporters (PTR2)	29.23 4.18e-23 67-119
1374	PR00308C	Type I antifreeze protein signature III	2.79 2.78e-09 20-29
1374	PR01471B	Histamine H3 receptor signature II	12.38 9.63e-09 24-42
1375	IPB000169A	Eukaryotic thiol (cysteine) proteases active site	10.17 1.00e-14 132-141
1375	IPB000169C	Eukaryotic thiol (cysteine) proteases active site	8.11 2.93e-11 274-284
1375	IPB000169D	Eukaryotic thiol (cysteine) proteases active site	8.56 9.44e-19 295-311
1375	PR00704C	Calpain cysteine protease (C2) family signature III	11.35 6.01e-09 132-148
1375	PR00705A	Papain cysteine protease (C1) family signature I	11.22 2.80e-21 132-147
1375	PR00705B	Papain cysteine protease (C1) family signature II	10.02 1.45e-10 276-286
1375	PR00705C	Papain cysteine protease (C1) family signature III	13.28 1.00e-09 295-301
1376	IPB000276A	Rhodopsin-like GPCR superfamily	11.56 9.05e-10 125-136
1376	IPB000276B	Rhodopsin-like GPCR superfamily	4.97 5.74e-09 201-212
1376	PR00237B	Rhodopsin-like GPCR superfamily signature II	12.45 7.87e-09 66-87
1376	PR00237C	Rhodopsin-like GPCR superfamily signature III	14.77 8.50e-12 111-133
1376	PR00237E	Rhodopsin-like GPCR superfamily signature V	13.03 4.21e-11 193-216
1376	PR00237F	Rhodopsin-like GPCR superfamily signature VI	14.34 4.55e-11 397-421
1376	PR00237G	Rhodopsin-like GPCR superfamily signature VII	19.23 6.09e-09 436-462

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1376	PR01103B	Adrenergic receptor signature II	13.72 2.50e-10 139-147
1378	IPB000203A	GPS domain	18.40 9.74e-09 209-239
1378	IPB000203B	GPS domain	13.98 3.25e-15 325-346
1378	IPB000832C	G-protein coupled receptors family 2 (secretin-like)	19.53 1.00e-10 325-354
1378	PR00249C	Secretin-like GPCR superfamily signature III	15.44 3.32e-09 327-350
1378	PR01380A	Claudin-5 signature I	5.16 8.79e-09 265-273
1380	IPB002190A	MAGE family	31.63 4.40e-18 1-37
1380	IPB002190B	MAGE family	27.39 1.61e-26 109-153
1380	IPB002190C	MAGE family	33.01 9.12e-31 179-233
1380	IPB002190D	MAGE family	18.35 1.00e-40 239-288
1381	PR00169G	Potassium channel signature VII	11.30 6.38e-09 265-287
1381	PR01320B	Inward rectifier K ⁺ channel superfamily signature II	12.73 7.46e-11 162-184
1381	PR01333A	Two pore domain K ⁺ channel signature I	18.74 8.11e-28 168-196
1381	PR01333B	Two pore domain K ⁺ channel signature II	10.39 2.58e-09 171-180
1381	PR01333B	Two pore domain K ⁺ channel signature II	10.39 7.10e-10 280-289
1381	PR01463F	EAG/ELK/ERG potassium channel family signature VI	4.09 3.42e-09 268-285
1381	PR01499A	Trek K ⁺ channel signature I	8.28 7.99e-12 21-34
1381	PR01499B	Trek K ⁺ channel signature II	9.88 8.15e-21 68-85
1381	PR01499C	Trek K ⁺ channel signature III	9.14 7.07e-14 105-117
1381	PR01499D	Trek K ⁺ channel signature IV	8.87 9.05e-20 119-137
1381	PR01499E	Trek K ⁺ channel signature V	14.43 2.73e-14 146-158
1381	PR01499F	Trek K ⁺ channel signature VI	10.57 1.00e-24 196-215
1381	PR01499G	Trek K ⁺ channel signature VII	12.38 7.80e-22 216-235
1381	PR01499H	Trek K ⁺ channel signature VIII	9.00 6.71e-14 237-248
1381	PR01499I	Trek K ⁺ channel signature IX	11.15 4.73e-20 293-308
1381	PR01499J	Trek K ⁺ channel signature X	16.62 1.11e-16 315-326
1381	PR01499K	Trek K ⁺ channel signature XI	11.81 2.96e-20 328-344
1381	PR01499L	Trek K ⁺ channel signature XII	13.04 4.80e-17 364-378
1382	IPB000920C	Myelin P0 protein	15.78 6.50e-09 245-297
1382	IPB003784	BioY	27.20 1.22e-09 263-313
1382	PR00213E	Myelin P0 protein signature V	5.51 8.97e-09 263-287
1382	PR01228C	Eggshell protein signature III	5.69 5.14e-09 306-321
1385	IPB001039A	Major histocompatibility complex protein, Class I	17.17 8.89e-11 19-72
1388	IPB002130A	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	13.87 1.53e-18 58-79
1388	IPB002130B	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	21.20 2.93e-37 88-126
1388	IPB002130C	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	16.92 9.50e-34 138-175
1388	PR00153A	Cyclophilin peptidyl-prolyl cis-trans isomerase signature I	14.60 1.00e-15 64-79
1388	PR00153B	Cyclophilin peptidyl-prolyl cis-trans isomerase signature II	12.94 5.24e-17 93-105
1388	PR00153C	Cyclophilin peptidyl-prolyl cis-trans isomerase signature III	10.79 1.00e-17 136-151
1388	PR00153D	Cyclophilin peptidyl-prolyl cis-trans isomerase signature IV	10.73 7.75e-16 151-163
1388	PR00153E	Cyclophilin peptidyl-prolyl cis-trans isomerase signature V	8.39 5.15e-10 164-179

Table 3B

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SEQ ID NO:	Database entry ID	Description	Results*
1390	IPB000276B	Rhodopsin-like GPCR superfamily	4.97 6.06e-10 102-113
1390	IPB000276C	Rhodopsin-like GPCR superfamily	8.03 8.50e-11 162-173
1390	PR00237D	Rhodopsin-like GPCR superfamily signature IV	9.76 4.38e-09 58-79
1390	PR00237E	Rhodopsin-like GPCR superfamily signature V	13.03 6.50e-15 94-117
1390	PR00237F	Rhodopsin-like GPCR superfamily signature VI	14.34 5.91e-15 152-176
1390	PR00237G	Rhodopsin-like GPCR superfamily signature VII	19.23 5.70e-09 192-218
1390	PR00529D	Gonadotrophin releasing hormone receptor signature IV	22.60 7.38e-13 2-17
1390	PR00529F	Gonadotrophin releasing hormone receptor signature VI	5.71 5.09e-10 75-89
1390	PR00529H	Gonadotrophin releasing hormone receptor signature VIII	9.64 9.43e-11 176-196
1392	IPB003662A	General substrate transporters	18.97 8.76e-13 196-228
1393	IPB000276A	Rhodopsin-like GPCR superfamily	11.56 1.69e-13 157-168
1393	PR00237C	Rhodopsin-like GPCR superfamily signature III	14.77 3.84e-10 143-165
1393	PR00245B	Olfactory receptor signature II	13.73 6.54e-11 168-180
1393	PR00245C	Olfactory receptor signature III	14.65 3.75e-11 215-231
1393	PR00245E	Olfactory receptor signature V	8.96 7.91e-10 322-333
1397	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 6.88e-09 294-331
1397	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 8.92e-10 487-524
1397	IPB003529B	Long hematopoietin receptor, gp130 family	20.65 2.31e-09 646-668
1397	PR00014C	Fibronectin type III repeat signature III	14.47 8.71e-09 585-603
1397	PR00014D	Fibronectin type III repeat signature IV	15.12 2.96e-09 1023-1037
1397	PR00014D	Fibronectin type III repeat signature IV	15.12 9.22e-09 701-715
1402	IPB000195B	RabGAP/TBC domain	14.35 5.15e-09 38-50
1402	PR00250G	Fungal pheromone mating factor STE2 GPCR signature VII	9.58 9.75e-09 21-42
1409	IPB001359H	Synapsin	22.58 9.63e-10 53-103
1409	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 1.43e-13 297-334
1409	IPB003531C	Short hematopoietin receptor family 1	15.87 9.38e-11 543-560
1413	PR01131B	Connexin36 (Cx36) signature II	3.45 2.41e-09 500-512
1414	IPB001993A	Mitochondrial energy transfer proteins (carrier protein)	16.91 7.00e-11 143-167
1414	IPB001993A	Mitochondrial energy transfer proteins (carrier protein)	16.91 7.50e-18 46-70
1414	IPB001993B	Mitochondrial energy transfer proteins (carrier protein)	9.00 5.15e-14 182-195
1414	PR00927E	Adenine nucleotide translocator 1 signature V	14.99 6.33e-09 74-95
1416	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 1.00e-09 6-43
1416	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 7.92e-09 88-125
1417	IPB000315A	B-box zinc finger superfamily	24.51 3.25e-10 30-53
1417	IPB001841	RING finger	10.69 1.56e-10 42-51
1418	IPB001285A	Synaptophysin/synaptoporin	12.19 1.00e-28 41-87

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SEQ ID NO:	Database entry ID	Description	Results*
1418	IPB001285C	Synaptophysin/synaptoporin	15.24 9.89e-23 125-165
1418	IPB001285D	Synaptophysin/synaptoporin	12.74 4.03e-13 166-200
1418	IPB001285E	Synaptophysin/synaptoporin	9.55 2.98e-24 201-247
1418	PR00220A	Synaptophysin/synaptoporin family signature I	13.69 7.60e-26 38-60
1418	PR00220B	Synaptophysin/synaptoporin family signature II	17.03 5.35e-23 62-87
1418	PR00220C	Synaptophysin/synaptoporin family signature III	11.86 2.85e-25 117-141
1418	PR00220D	Synaptophysin/synaptoporin family signature IV	10.60 6.84e-25 149-172
1418	PR00220E	Synaptophysin/synaptoporin family signature V	4.56 4.60e-23 216-234
1418	PR00489C	Frizzled protein signature III	8.19 2.36e-09 216-240
1419	IPB000729B	PMP-22/EMP/MP20 family	13.56 4.86e-11 49-59
1419	IPB000729C	PMP-22/EMP/MP20 family	37.83 9.01e-15 80-132
1419	IPB000729C	PMP-22/EMP/MP20 family	37.83 9.72e-10 87-139
1421	IPB001905A	Ammonium transporter family	22.03 8.47e-14 69-97
1421	IPB001905B	Ammonium transporter family	19.59 6.08e-17 127-159
1421	IPB001905C	Ammonium transporter family	15.52 5.35e-18 178-203
1421	IPB001905D	Ammonium transporter family	11.89 3.61e-19 217-240
1421	IPB001905F	Ammonium transporter family	17.91 1.00e-18 287-313
1421	PR00342B	Rhesus blood group protein signature II	14.04 5.57e-13 61-78
1421	PR00342C	Rhesus blood group protein signature III	11.52 5.03e-11 90-107
1421	PR00342D	Rhesus blood group protein signature IV	11.18 8.69e-13 128-144
1421	PR00342E	Rhesus blood group protein signature V	17.96 3.74e-10 151-174
1421	PR00342F	Rhesus blood group protein signature VI	8.73 3.88e-10 185-200
1421	PR00342G	Rhesus blood group protein signature VII	10.10 2.70e-20 220-238
1421	PR00342H	Rhesus blood group protein signature VIII	8.86 1.76e-12 250-272
1423	IPB001427A	Pancreatic ribonuclease family	12.97 5.09e-10 36-45
1423	IPB001427B	Pancreatic ribonuclease family	31.44 6.04e-34 50-100
1423	IPB001427C	Pancreatic ribonuclease family	24.33 2.17e-13 106-136
1423	PR00794A	Pancreatic ribonuclease family signature I	15.68 6.31e-13 51-70
1423	PR00794B	Pancreatic ribonuclease family signature II	17.91 6.34e-13 71-90
1423	PR00794C	Pancreatic ribonuclease family signature III	16.87 8.07e-14 96-114
1423	PR00794D	Pancreatic ribonuclease family signature IV	19.74 2.37e-09 117-139
1426	IPB000038A	Cell division/GTP binding protein	16.77 9.89e-09 447-488
1426	IPB001984C	ATP-dependent serine proteases, Lon family	12.76 3.32e-09 158-194
1426	PR00318A	Alpha G protein (transducin) signature I	6.88 5.19e-10 469-484
1426	PR00830A	Endopeptidase La (Lon) serine protease (S16) signature I	8.52 2.14e-11 165-184
1426	PR01100A	Shikimate kinase family signature I	8.30 1.00e-08 470-485
1427	IPB000483	Leucine rich repeat C-terminal domain	11.18 6.85e-13 164-178
1427	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 8.20e-10 259-296
1427	PR00019A	Leucine-rich repeat signature I	11.72 3.18e-09 52-65
1427	PR00019A	Leucine-rich repeat signature I	11.72 5.64e-09 77-90
1427	PR00019B	Leucine-rich repeat signature II	11.42 1.27e-09 25-38
1427	PR00019B	Leucine-rich repeat signature II	11.42 4.82e-09 49-62
1427	PR00019B	Leucine-rich repeat signature II	11.42 6.32e-11 74-87
1430	PR00462B	Fungal lignin peroxidase family signature II	14.83 4.74e-09 34-52
1435	IPB002610A	Rhomboid family	5.73 9.50e-10 185-194
1437	IPB001627A	Sema domain	16.97 9.34e-09 138-153

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1437	IPB001627C	Sema domain	21.13 7.11e-09 201-232
1437	IPB001627D	Sema domain	16.04 9.47e-17 249-264
1437	IPB001627F	Sema domain	22.05 8.50e-27 293-326
1437	IPB001627G	Sema domain	21.49 5.36e-22 346-379
1437	IPB001627J	Sema domain	11.43 2.97e-14 462-478
1437	IPB001627K	Sema domain	13.76 4.00e-14 540-552
1437	IPB002165A	Plexin repeat	15.07 3.73e-12 138-153
1437	IPB002165B	Plexin repeat	13.59 3.43e-12 175-184
1437	IPB002165C	Plexin repeat	18.49 6.32e-34 293-325
1437	IPB002165D	Plexin repeat	14.72 2.85e-15 540-552
1437	IPB002861B	Reeler domain	10.50 3.56e-09 890-918
1437	IPB002861B	Reeler domain	10.50 9.76e-12 644-672
1437	PR01303D	Plasmodium circumsporozoite protein signature IV	10.57 2.50e-09 708-725
1438	PR00170A	Voltage-gated Na ⁺ channel alpha subunit signature I	8.35 3.04e-10 800-819
1438	PR01097A	Transient receptor potential family signature I	11.54 5.06e-09 799-820
1439	PR00170A	Voltage-gated Na ⁺ channel alpha subunit signature I	8.35 3.04e-10 881-900
1439	PR01097A	Transient receptor potential family signature I	11.54 5.06e-09 880-901
1442	IPB000483	Leucine rich repeat C-terminal domain	11.18 6.73e-12 186-200
1442	PR00019A	Leucine-rich repeat signature I	11.72 1.33e-10 106-119
1443	IPB000135A	High mobility group proteins HMG1 and HMG2	11.69 2.69e-31 34-88
1443	IPB000135B	High mobility group proteins HMG1 and HMG2	13.24 3.78e-24 88-132
1443	IPB000203A	GPS domain	18.40 8.43e-09 126-156
1443	IPB000203B	GPS domain	13.98 4.95e-12 286-307
1443	IPB000832C	G-protein coupled receptors family 2 (secretin-like)	19.53 4.64e-14 286-315
1443	PR00249C	Secretin-like GPCR superfamily signature III	15.44 9.56e-10 288-311
1443	PR00249D	Secretin-like GPCR superfamily signature IV	14.10 9.44e-09 327-352
1443	PR00886A	High mobility group (HMG1/HMG2) protein signature I	10.57 8.29e-17 37-59
1443	PR00886B	High mobility group (HMG1/HMG2) protein signature II	10.07 8.97e-13 60-80
1443	PR00886C	High mobility group (HMG1/HMG2) protein signature III	11.20 1.40e-11 104-122
1448	IPB002000D	Lysosome-associated membrane glycoprotein (Lamp)	5.87 5.75e-09 419-432
1448	PR00308C	Type I antifreeze protein signature III	2.79 9.64e-09 758-767
1449	PR00180B	Cellular retinaldehyde-binding protein signature II	15.78 8.03e-09 236-260
1452	IPB001993A	Mitochondrial energy transfer proteins (carrier protein)	16.91 8.65e-10 33-57
1452	IPB001993A	Mitochondrial energy transfer proteins (carrier protein)	16.91 9.39e-09 130-154
1452	IPB001993B	Mitochondrial energy transfer proteins (carrier protein)	9.00 4.21e-09 78-91
1452	IPB001993B	Mitochondrial energy transfer proteins	9.00 7.14e-11 173-186

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
		(carrier protein)	
1452	PR00926D	Mitochondrial carrier protein signature IV	10.86 7.92e-17 41-59
1452	PR00926E	Mitochondrial carrier protein signature V	11.83 5.74e-19 89-107
1452	PR00926F	Mitochondrial carrier protein signature VI	17.31 1.00e-09 35-57
1452	PR00926F	Mitochondrial carrier protein signature VI	17.31 5.76e-24 132-154
1452	PR00927A	Adenine nucleotide translocator 1 signature I	7.76 8.53e-09 28-40
1452	PR00927B	Adenine nucleotide translocator 1 signature II	15.15 1.44e-12 164-185
1452	PR00927D	Adenine nucleotide translocator 1 signature IV	10.82 3.79e-13 26-39
1452	PR00927E	Adenine nucleotide translocator 1 signature V	14.99 6.32e-11 162-183
1452	PR00927E	Adenine nucleotide translocator 1 signature V	14.99 9.25e-22 67-88
1452	PR00927F	Adenine nucleotide translocator 1 signature VI	12.47 5.50e-14 128-144
1452	PR00927G	Adenine nucleotide translocator 1 signature VII	10.67 5.14e-15 178-193
1454	IPB001993A	Mitochondrial energy transfer proteins (carrier protein)	16.91 8.75e-11 83-107
1454	IPB001993B	Mitochondrial energy transfer proteins (carrier protein)	9.00 1.72e-10 242-255
1455	PR00320A	G protein beta WD-40 repeat signature I	13.15 1.96e-09 128-142
1455	PR00320C	G protein beta WD-40 repeat signature III	12.32 3.67e-09 128-142
1456	IPB000494A	Epidermal growth-factor receptor (EGFR), L domain	22.80 6.59e-25 122-154
1456	IPB000494B	Epidermal growth-factor receptor (EGFR), L domain	24.47 6.00e-18 228-248
1456	IPB000494C	Epidermal growth-factor receptor (EGFR), L domain	24.40 9.45e-33 1099-1145
1456	IPB000494D	Epidermal growth-factor receptor (EGFR), L domain	19.44 1.00e-40 1162-1211
1456	IPB000494E	Epidermal growth-factor receptor (EGFR), L domain	21.65 3.53e-27 1218-1253
1456	IPB001060C	Cell division control protein 15 (CDC15)	26.16 1.00e-09 1183-1202
1456	IPB001245A	Tyrosine kinase catalytic domain	22.45 4.27e-19 1105-1145
1456	IPB001245B	Tyrosine kinase catalytic domain	21.68 6.54e-29 1165-1203
1456	IPB001772C	Kinase associated domain 1	20.66 1.75e-10 1100-1130
1456	IPB002174A	Furin-like cysteine rich region	30.51 4.41e-13 126-157
1456	IPB002174B	Furin-like cysteine rich region	11.91 7.00e-10 1183-1193
1456	IPB003961B	Fibronectin type III domain	12.29 7.43e-11 1184-1194
1456	PR00014D	Fibronectin type III repeat signature IV	15.12 6.09e-09 893-907
1456	PR00109A	Tyrosine kinase catalytic domain signature I	12.56 5.34e-11 1066-1079
1456	PR00109B	Tyrosine kinase catalytic domain signature II	11.07 1.47e-20 1112-1130
1456	PR00109C	Tyrosine kinase catalytic domain signature III	11.86 9.25e-13 1164-1174
1456	PR00109D	Tyrosine kinase catalytic domain signature IV	17.61 4.50e-24 1183-1205
1456	PR00109E	Tyrosine kinase catalytic domain signature V	12.99 4.48e-16 1227-1249
1457	IPB002889B	WSC domain	11.76 8.41e-09 1558-1604
1462	IPB000130	Neutral zinc metalloproteases, zinc-	5.86 4.00e-12 238-248

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
		binding region	
1462	IPB001818A	Matrixin	14.60 2.13e-29 91-120
1462	IPB001818B	Matrixin	26.48 6.04e-31 137-178
1462	IPB001818C	Matrixin	24.38 4.09e-32 20-65
1462	IPB001818C	Matrixin	24.38 7.43e-35 182-227
1462	IPB001818D	Matrixin	14.91 3.08e-37 232-263
1462	IPB001818E	Matrixin	8.86 7.19e-15 273-286
1462	IPB001818F	Matrixin	11.19 6.36e-13 309-329
1462	PR00138A	Matrixin signature I	12.54 1.64e-16 111-124
1462	PR00138B	Matrixin signature II	14.84 5.21e-10 156-171
1462	PR00138C	Matrixin signature III	20.07 1.78e-16 180-208
1462	PR00138C	Matrixin signature III	20.07 8.38e-15 18-46
1462	PR00138D	Matrixin signature IV	14.57 5.50e-31 238-263
1462	PR00138E	Matrixin signature V	7.10 8.71e-15 273-286
1462	PR00480B	Astacin family signature II	14.35 1.16e-11 233-251
1462	PR00997G	Fragilysin metalloproteinase (M10C) enterotoxin signature VII	11.64 8.01e-10 244-260
1466	IPB000008D	C2 domain	14.83 5.92e-09 288-306
1466	PR01471E	Histamine H3 receptor signature V	5.41 2.43e-10 610-625
1468	IPB000228D	RNA 3'-terminal phosphate cyclase	33.18 4.89e-19 30-67
1468	IPB000228E	RNA 3'-terminal phosphate cyclase	26.21 8.43e-09 105-146
1468	IPB002029A	Aspartate and ornithine carbamoyltransferase family	20.73 7.86e-09 78-105
1470	IPB003874C	CDC45-like protein	5.49 9.16e-10 315-326
1473	IPB002568A	Carlavirus putative nucleic acid binding protein	12.57 9.66e-09 9-34
1473	IPB002999B	Tudor domain	7.50 5.09e-09 29-37
1473	IPB003482B	Transcription factor WhiB	10.09 5.73e-09 10-22
1474	PR01547I	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature IX	15.37 7.94e-28 69-99
1474	PR01547K	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature XI	13.61 7.00e-15 95-114
1474	PR01547L	Saccharomyces cerevisiae 175.8kDa hypothetical protein signature XII	10.35 6.29e-19 119-135
1477	IPB000822	Zinc finger, C2H2 type	14.67 2.88e-09 421-446
1477	PR01407E	Butyrophilin C-terminal DUF signature V	13.29 1.63e-09 56-80
1478	IPB001925C	Eukaryotic porin	23.55 1.84e-28 8-61
1478	PR00185D	Eukaryotic porin signature IV	14.33 9.50e-12 111-128
1482	PR00449E	Transforming protein P21 ras signature V	13.39 1.29e-11 464-486
1489	IPB003859B	Metazoa galactosyltransferase	27.85 8.27e-18 205-257
1489	IPB003859C	Metazoa galactosyltransferase	19.53 3.74e-36 301-335
1489	IPB003859D	Metazoa galactosyltransferase	26.76 6.25e-27 349-382
1491	IPB003191M	Guanylate-binding protein	10.38 7.86e-28 28-58
1491	IPB003191N	Guanylate-binding protein	9.33 6.16e-21 61-91
1491	IPB003191O	Guanylate-binding protein	14.31 7.22e-28 92-132
1491	IPB003191O	Guanylate-binding protein	14.31 8.23e-09 81-121
1493	PR00502B	NUDIX hydrolase family signature II	14.82 4.15e-09 348-363
1494	IPB000117D	Kappa casein	10.18 8.71e-09 117-151
1497	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 3.00e-15 88-125
1498	IPB001395E	Aldo/keto reductase family	20.87 7.39e-23 256-293
1498	IPB001395F	Aldo/keto reductase family	25.03 2.45e-23 317-362
1498	PR00069D	Aldo-keto reductase signature IV	19.00 3.92e-20 260-289
1499	IPB000237B	GRIP domain	30.66 8.24e-09 543-593

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SEQ ID NO:	Database entry ID	Description	Results*
1499	IPB000237B	GRIP domain	30.66 8.34e-09 547-597
1499	IPB000996B	Clathrin light chain	20.25 7.55e-09 541-593
1499	IPB001800D	Lipoprotein, type 6	22.73 9.11e-09 558-604
1499	IPB001800D	Lipoprotein, type 6	22.73 9.70e-09 563-609
1499	IPB002101B	MARCKS family	14.58 2.28e-09 545-596
1499	IPB002906A	Ribosomal protein S27a	11.48 3.00e-09 561-593
1499	IPB002906A	Ribosomal protein S27a	11.48 9.81e-10 558-590
1499	IPB003121A	BAF60b domain of the SWIB complex	13.89 9.46e-09 552-577
1499	IPB003134F	Repeat in HS1/Cortactin	15.66 8.49e-09 552-600
1503	PR00049D	Wilm's tumour protein signature IV	0.00 9.57e-10 65-79
1503	PR01217B	Proline rich extensin signature II	4.82 8.55e-09 71-87
1504	IPB000436B	Sushi domain / SCR repeat / CCP module	8.70 8.71e-10 307-318
1504	PR01544D	Arabidopsis thaliana 130.7kDa hypothetical protein signature IV	14.54 9.13e-10 373-394
1511	IPB000822	Zinc finger, C2H2 type	14.67 3.77e-18 343-368
1511	IPB000822	Zinc finger, C2H2 type	14.67 9.25e-19 371-396
1511	IPB001275	DM DNA binding domain	19.17 3.51e-09 331-370
1511	IPB001275	DM DNA binding domain	19.17 5.67e-09 359-398
1511	IPB001909	KRAB box	17.37 4.00e-19 230-264
1511	PR00048A	C2H2-type zinc finger signature I	9.94 5.76e-12 368-381
1511	PR00048A	C2H2-type zinc finger signature I	9.94 7.75e-16 340-353
1511	PR00048B	C2H2-type zinc finger signature II	5.52 7.43e-10 384-393
1517	IPB000822	Zinc finger, C2H2 type	14.67 1.00e-17 1066-1091
1517	IPB000822	Zinc finger, C2H2 type	14.67 1.00e-19 281-306
1517	IPB000822	Zinc finger, C2H2 type	14.67 1.60e-16 393-418
1517	IPB000822	Zinc finger, C2H2 type	14.67 1.60e-16 954-979
1517	IPB000822	Zinc finger, C2H2 type	14.67 1.69e-18 477-502
1517	IPB000822	Zinc finger, C2H2 type	14.67 2.13e-14 1038-1063
1517	IPB000822	Zinc finger, C2H2 type	14.67 4.79e-12 1094-1119
1517	IPB000822	Zinc finger, C2H2 type	14.67 5.50e-19 421-446
1517	IPB000822	Zinc finger, C2H2 type	14.67 5.50e-20 870-895
1517	IPB000822	Zinc finger, C2H2 type	14.67 6.73e-21 926-951
1517	IPB000822	Zinc finger, C2H2 type	14.67 7.00e-20 309-334
1517	IPB000822	Zinc finger, C2H2 type	14.67 8.36e-21 337-362
1517	IPB000822	Zinc finger, C2H2 type	14.67 8.36e-21 982-1007
1517	IPB000822	Zinc finger, C2H2 type	14.67 8.50e-20 449-474
1517	IPB000822	Zinc finger, C2H2 type	14.67 9.25e-20 898-923
1517	IPB000822	Zinc finger, C2H2 type	14.67 9.31e-18 1010-1035
1517	IPB000822	Zinc finger, C2H2 type	14.67 9.40e-16 365-390
1517	IPB000822	Zinc finger, C2H2 type	14.67 9.44e-15 505-530
1517	IPB001275	DM DNA binding domain	19.17 1.12e-10 970-1009
1517	IPB001275	DM DNA binding domain	19.17 3.55e-10 297-336
1517	IPB001275	DM DNA binding domain	19.17 3.69e-12 437-476
1517	IPB001275	DM DNA binding domain	19.17 4.19e-09 886-925
1517	IPB001275	DM DNA binding domain	19.17 4.19e-09 942-981
1517	IPB001275	DM DNA binding domain	19.17 6.71e-13 325-364
1517	IPB001275	DM DNA binding domain	19.17 6.72e-10 1082-1121
1517	IPB001275	DM DNA binding domain	19.17 6.72e-10 914-953
1517	IPB001275	DM DNA binding domain	19.17 8.06e-09 858-897
1517	IPB001275	DM DNA binding domain	19.17 8.18e-10 998-1037
1517	IPB001275	DM DNA binding domain	19.17 9.10e-11 1026-1065
1517	IPB001275	DM DNA binding domain	19.17 9.88e-10 465-504
1517	IPB001909	KRAB box	17.37 8.03e-18 675-709

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SEQ ID NO:	Database entry ID	Description	Results*
1517	IPB001909	KRAB box	17.37 9.00e-32 76-110
1517	PR00048A	C2H2-type zinc finger signature I	9.94 1.69e-14 306-319
1517	PR00048A	C2H2-type zinc finger signature I	9.94 1.90e-15 446-459
1517	PR00048A	C2H2-type zinc finger signature I	9.94 2.42e-11 474-487
1517	PR00048A	C2H2-type zinc finger signature I	9.94 2.93e-13 502-515
1517	PR00048A	C2H2-type zinc finger signature I	9.94 3.08e-14 1035-1048
1517	PR00048A	C2H2-type zinc finger signature I	9.94 4.38e-09 1007-1020
1517	PR00048A	C2H2-type zinc finger signature I	9.94 5.50e-13 334-347
1517	PR00048A	C2H2-type zinc finger signature I	9.94 5.50e-13 895-908
1517	PR00048A	C2H2-type zinc finger signature I	9.94 6.14e-13 923-936
1517	PR00048A	C2H2-type zinc finger signature I	9.94 7.00e-09 867-880
1517	PR00048A	C2H2-type zinc finger signature I	9.94 7.35e-12 362-375
1517	PR00048A	C2H2-type zinc finger signature I	9.94 7.55e-10 390-403
1517	PR00048A	C2H2-type zinc finger signature I	9.94 8.11e-11 979-992
1517	PR00048A	C2H2-type zinc finger signature I	9.94 8.58e-11 418-431
1517	PR00048A	C2H2-type zinc finger signature I	9.94 9.05e-11 951-964
1517	PR00048A	C2H2-type zinc finger signature I	9.94 9.36e-13 1091-1104
1517	PR00048B	C2H2-type zinc finger signature II	5.52 1.00e-09 911-920
1517	PR00048B	C2H2-type zinc finger signature II	5.52 2.29e-10 939-948
1517	PR00048B	C2H2-type zinc finger signature II	5.52 2.50e-09 995-1004
1517	PR00048B	C2H2-type zinc finger signature II	5.52 2.93e-10 350-359
1517	PR00048B	C2H2-type zinc finger signature II	5.52 3.25e-11 294-303
1517	PR00048B	C2H2-type zinc finger signature II	5.52 3.25e-11 434-443
1517	PR00048B	C2H2-type zinc finger signature II	5.52 3.25e-11 883-892
1517	PR00048B	C2H2-type zinc finger signature II	5.52 3.57e-10 1023-1032
1517	PR00048B	C2H2-type zinc finger signature II	5.52 6.00e-09 462-471
1517	PR00048B	C2H2-type zinc finger signature II	5.52 7.00e-09 967-976
1518	IPB000353B	Class II histocompatibility antigen, beta chain, beta-1 domain	19.16 2.63e-13 21-70
1518	IPB000353C	Class II histocompatibility antigen, beta chain, beta-1 domain	20.11 1.41e-10 71-125
1518	IPB001003B	MHC Class II, alpha chain, alpha-1 domain	14.72 4.45e-09 29-72
1518	IPB003006A	Immunoglobulin and major histocompatibility complex domain	17.51 1.00e-13 42-64
1518	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 9.40e-19 78-115
1518	PR01436D	NADH-ubiquinone oxidoreductase chain 2 signature IV	4.56 2.66e-09 6-18
1521	IPB001618	Coenzyme A transferase	37.23 1.86e-09 56-109
1521	IPB001618	Coenzyme A transferase	37.23 5.75e-32 355-408
1521	IPB001618	Coenzyme A transferase	37.23 6.92e-31 196-249
1521	IPB001839A	Transforming growth factor (TGF) beta family	12.37 3.81e-17 657-673
1521	IPB001839B	Transforming growth factor (TGF) beta family	11.15 2.17e-12 704-718
1521	IPB001839C	Transforming growth factor (TGF) beta family	12.59 2.80e-16 724-741
1521	PR00438A	Growth factor cystine knot domain signature I	11.01 4.00e-09 665-674
1521	PR00669E	Inhibin alpha chain signature V	14.95 5.39e-12 640-657
1523	IPB000034A	Laminin B	22.21 8.56e-09 661-696
1523	IPB001762A	Disintegrin	23.93 4.21e-21 453-493
1523	IPB001762B	Disintegrin	10.06 7.30e-13 500-510
1523	IPB002870A	Reprolysin family propeptide	12.22 6.54e-09 109-125

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SEQ ID NO:	Database entry ID	Description	Results*
1523	IPB002870B	Reprolysin family propeptide	24.73 9.38e-26 154-192
1523	IPB002870D	Reprolysin family propeptide	16.31 6.33e-11 323-338
1523	IPB002870E	Reprolysin family propeptide	11.90 7.57e-12 355-367
1523	IPB002870F	Reprolysin family propeptide	18.81 6.85e-19 398-422
1523	IPB003854B	Gibberellin regulated protein	19.26 4.69e-09 470-508
1523	PR00289A	Disintegrin signature I	14.29 2.55e-14 469-488
1523	PR00289B	Disintegrin signature II	11.74 7.27e-10 498-510
1524	IPB000387	Tyrosine specific protein phosphatase and dual specificity protein phosphatase family	10.77 5.00e-11 186-196
1524	IPB001073A	Complement C1q protein	22.14 5.50e-09 249-283
1524	IPB001073A	Complement C1q protein	22.14 5.50e-09 436-470
1524	IPB001695C	Lysyl oxidase	12.69 2.64e-09 391-415
1524	PR00700D	Protein tyrosine phosphatase signature IV	12.83 5.79e-10 183-201
1525	IPB000276C	Rhodopsin-like GPCR superfamily	8.03 4.52e-09 5-16
1525	IPB000276D	Rhodopsin-like GPCR superfamily	9.40 5.24e-14 45-61
1525	PR00237G	Rhodopsin-like GPCR superfamily signature VII	19.23 8.77e-17 35-61
1525	PR00424F	Adenosine receptor signature VI	8.75 5.34e-12 35-45
1525	PR00554F	Adenosine A2B receptor signature VI	8.86 1.75e-16 24-36
1525	PR00554G	Adenosine A2B receptor signature VII	14.18 7.29e-12 69-88
1527	IPB001045B	Spermidine synthase	18.40 1.35e-12 314-356
1528	IPB002048	EF-hand family	7.91 4.32e-09 338-350
1528	PR01286E	Orphan nuclear receptor NOR1 signature V	5.27 6.65e-09 6-27
1528	PR01362H	Flagellar calcium-binding protein (calflagin) signature VIII	4.86 7.13e-09 150-166
1532	IPB001602A	Uncharacterized protein family UPF0047	15.98 8.94e-10 119-137
1534	IPB003861B	E4 protein	9.06 2.96e-09 1051-1065
1534	PR00021A	Small proline-rich protein signature I	3.31 4.55e-09 1044-1056
1535	IPB001359H	Synapsin	22.58 6.59e-09 39-89
1535	PR00671C	Inhibin beta B chain signature III	4.18 9.69e-09 44-63
1538	IPB000095F	PAK-box /P21-Rho-binding	16.47 3.95e-09 146-200
1538	IPB000861G	PKN/rhophilin/rhotekin rho-binding repeat	13.73 9.15e-11 144-193
1538	IPB000959D	POLO box duplicated region	27.01 6.72e-09 196-248
1538	IPB000961D	Protein kinase C-terminal domain	21.23 2.00e-14 138-179
1538	IPB001245A	Tyrosine kinase catalytic domain	22.45 6.63e-16 82-122
1538	IPB001245B	Tyrosine kinase catalytic domain	21.68 7.55e-17 142-180
1538	IPB001772C	Kinase associated domain 1	20.66 9.73e-16 77-107
1538	IPB001772D	Kinase associated domain 1	21.67 4.67e-09 149-188
1538	IPB001772E	Kinase associated domain 1	24.88 2.67e-10 203-242
1538	IPB003527D	MAP kinase	21.53 2.04e-09 135-176
1538	IPB003527G	MAP kinase	17.26 2.38e-09 215-252
1539	PR00502B	NUDIX hydrolase family signature II	14.82 7.53e-09 131-146
1540	IPB000777A	Envelope glycoprotein GP120	12.67 9.67e-09 652-665
1540	IPB000822	Zinc finger, C2H2 type	14.67 9.57e-10 729-754
1540	IPB003036C	Gag P30 core shell protein	11.53 4.86e-09 799-815
1540	PR00049D	Wilm's tumour protein signature IV	0.00 1.79e-10 813-827
1541	IPB000885A	Fibrillar collagen C-terminal domain	11.46 1.00e-12 537-574
1541	IPB000885A	Fibrillar collagen C-terminal domain	11.46 2.52e-11 534-571
1541	IPB000885A	Fibrillar collagen C-terminal domain	11.46 2.56e-09 543-580
1541	IPB000885A	Fibrillar collagen C-terminal domain	11.46 5.85e-11 546-583
1541	IPB000885A	Fibrillar collagen C-terminal domain	11.46 6.69e-09 555-592
1541	IPB000885A	Fibrillar collagen C-terminal domain	11.46 7.27e-11 552-589
1541	IPB000885A	Fibrillar collagen C-terminal domain	11.46 7.36e-10 540-577

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SEQ ID NO:	Database entry ID	Description	Results*
1541	IPB000885A	Fibrillar collagen C-terminal domain	11.46 8.04e-10 528-565
1541	IPB000885A	Fibrillar collagen C-terminal domain	11.46 9.12e-10 549-586
1541	IPB000885A	Fibrillar collagen C-terminal domain	11.46 9.41e-10 531-568
1541	IPB000885B	Fibrillar collagen C-terminal domain	19.15 1.77e-10 520-573
1541	IPB000885B	Fibrillar collagen C-terminal domain	19.15 3.70e-09 547-600
1541	IPB000885B	Fibrillar collagen C-terminal domain	19.15 4.11e-09 538-591
1541	IPB000885B	Fibrillar collagen C-terminal domain	19.15 5.01e-09 544-597
1541	IPB000885B	Fibrillar collagen C-terminal domain	19.15 6.49e-10 517-570
1541	IPB000885B	Fibrillar collagen C-terminal domain	19.15 8.11e-10 523-576
1541	IPB000885B	Fibrillar collagen C-terminal domain	19.15 9.67e-09 541-594
1541	IPB000885C	Fibrillar collagen C-terminal domain	16.79 1.00e-40 639-678
1541	IPB000885D	Fibrillar collagen C-terminal domain	18.84 4.75e-32 728-765
1541	IPB000885E	Fibrillar collagen C-terminal domain	21.59 1.00e-40 800-841
1541	IPB001073A	Complement C1q protein	22.14 1.00e-08 554-588
1541	IPB001073A	Complement C1q protein	22.14 3.95e-09 551-585
1541	IPB001073A	Complement C1q protein	22.14 7.32e-13 548-582
1541	IPB001073A	Complement C1q protein	22.14 8.03e-09 542-576
1541	IPB001073A	Complement C1q protein	22.14 9.50e-11 545-579
1541	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 2.53e-12 548-600
1541	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 3.06e-10 551-603
1541	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 5.54e-09 527-579
1541	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 6.12e-10 545-597
1541	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 8.10e-10 542-594
1541	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 8.59e-09 524-576
1541	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 8.98e-09 536-588
1541	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 9.34e-10 521-573
1541	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 1.12e-09 546-566
1541	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 1.76e-12 549-569
1541	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 1.77e-10 552-572
1542	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 3.88e-11 1025-1035
1542	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 4.09e-10 927-942
1542	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 8.20e-18 1020-1035
1542	IPB000492B	Protamine 2 (PRM2)	5.26 9.27e-10 430-464
1542	IPB001862F	Membrane attack complex components/perforin/complement C9	29.39 5.39e-13 901-948
1542	IPB001881A	Calcium-binding EGF-like domain	8.72 3.40e-09 916-925
1542	IPB001881B	Calcium-binding EGF-like domain	12.28 7.00e-16 1020-1031
1542	IPB003886D	Extracellular domain in nidogen	13.91 2.77e-10 1020-1039
1542	PR00010A	Type II EGF-like signature I	12.91 2.64e-09 912-923
1542	PR00010C	Type II EGF-like signature III	6.98 1.58e-10 1025-1035

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SEQ ID NO:	Database entry ID	Description	Results*
1542	PR00010C	Type II EGF-like signature III	6.98 4.07e-09 932-942
1542	PR00011D	Type III EGF-like signature IV	12.12 2.54e-09 929-947
1542	PR00764F	Complement C9 signature VI	15.74 1.60e-10 918-938
1542	PR00907B	Thrombomodulin signature II	11.50 2.68e-10 1016-1032
1543	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 1.00e-11 88-125
1544	IPB001359H	Synapsin	22.58 2.49e-09 244-294
1544	IPB001394A	Ubiquitin carboxyl-terminal hydrolase family 2	12.64 8.00e-19 478-495
1544	IPB001394B	Ubiquitin carboxyl-terminal hydrolase family 2	17.87 3.16e-19 684-713
1544	IPB001394C	Ubiquitin carboxyl-terminal hydrolase family 2	8.52 1.00e-09 771-780
1544	IPB002000D	Lysosome-associated membrane glycoprotein (Lamp)	5.87 5.58e-09 241-254
1544	IPB002999B	Tudor domain	7.50 7.55e-09 244-252
1544	IPB002999B	Tudor domain	7.50 7.55e-09 245-253
1544	IPB002999B	Tudor domain	7.50 7.55e-09 246-254
1544	IPB003861B	E4 protein	9.06 1.00e-08 246-260
1544	IPB003861B	E4 protein	9.06 9.61e-09 251-265
1544	PR00049D	Wilm's tumour protein signature IV	0.00 1.29e-10 233-247
1544	PR00049D	Wilm's tumour protein signature IV	0.00 2.68e-09 243-257
1544	PR00049D	Wilm's tumour protein signature IV	0.00 4.05e-09 237-251
1544	PR00049D	Wilm's tumour protein signature IV	0.00 4.05e-09 238-252
1544	PR00049D	Wilm's tumour protein signature IV	0.00 4.05e-09 244-258
1544	PR00049D	Wilm's tumour protein signature IV	0.00 5.92e-11 242-256
1544	PR00049D	Wilm's tumour protein signature IV	0.00 6.75e-11 236-250
1544	PR00049D	Wilm's tumour protein signature IV	0.00 7.38e-12 239-253
1544	PR00049D	Wilm's tumour protein signature IV	0.00 8.01e-13 235-249
1544	PR00049D	Wilm's tumour protein signature IV	0.00 8.93e-10 241-255
1544	PR00049D	Wilm's tumour protein signature IV	0.00 9.39e-11 240-254
1544	PR00211B	Glutelin signature II	0.86 7.50e-09 238-258
1544	PR01102M	5-hydroxytryptamine 6 receptor signature XIII	11.13 6.32e-09 229-251
1544	PR01217G	Proline rich extensin signature VII	4.02 5.58e-09 233-258
1544	PR01471E	Histamine H3 receptor signature V	5.41 3.35e-09 235-250
1544	PR01471E	Histamine H3 receptor signature V	5.41 4.23e-09 236-251
1545	IPB001359H	Synapsin	22.58 3.80e-09 277-327
1545	IPB001359H	Synapsin	22.58 8.89e-10 437-487
1545	IPB001359H	Synapsin	22.58 9.83e-09 458-508
1545	IPB002999B	Tudor domain	7.50 2.64e-09 1028-1036
1546	PR00019B	Leucine-rich repeat signature II	11.42 4.33e-10 317-330
1546	PR00416B	Eukaryotic DNA topoisomerase I signature II	15.23 3.03e-09 389-408
1547	IPB000801A	Putative esterase	15.56 7.75e-09 522-533
1547	IPB003533C	Doublecortin	10.25 5.14e-10 627-670
1549	IPB001698A	F-actin capping protein beta subunit	11.94 2.89e-23 47-100
1549	PR00192A	F-actin capping protein beta subunit signature I	8.23 1.47e-27 47-67
1551	IPB002469G	Dipeptidyl peptidase IV, N-terminus	26.76 9.24e-11 362-400
1551	IPB002469H	Dipeptidyl peptidase IV, N-terminus	21.17 6.14e-16 407-442
1551	IPB002469I	Dipeptidyl peptidase IV, N-terminus	10.99 4.86e-16 452-470
1551	IPB002469J	Dipeptidyl peptidase IV, N-terminus	8.97 3.52e-12 534-550
1551	IPB002471B	Prolyl endopeptidase family serine active	24.90 3.66e-11 439-470

Table 3B

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SEQ ID NO:	Database entry ID	Description	Results*
		site	
1552	IPB000183D	Orn/DAP/Arg decarboxylases family 2	14.78 6.76e-12 38-57
1552	IPB000183E	Orn/DAP/Arg decarboxylases family 2	17.25 2.67e-09 106-129
1552	IPB000183G	Orn/DAP/Arg decarboxylases family 2	21.16 1.00e-17 171-191
1552	IPB003873C	Nonstructural protein NS3/small envelope protein E	7.97 8.03e-10 159-172
1552	PR00163B	Rubredoxin signature II	15.17 4.90e-09 143-159
1552	PR01179E	Ornithine/diaminopimelate/arginine (ODA) decarboxylase family signature V	16.24 5.06e-11 180-193
1552	PR01182G	Ornithine decarboxylase signature VII	11.35 7.00e-14 167-180
1558	IPB001331C	Guanine-nucleotide dissociation stimulators CDC24 family	16.09 2.40e-12 1104-1129
1558	IPB001478B	PDZ domain (also known as DHR or GLGF)	6.12 7.19e-09 198-207
1558	IPB002532J	Hantavirus glycoprotein G2	16.97 8.37e-09 1129-1165
1558	PR00049D	Wilm's tumour protein signature IV	0.00 4.81e-09 1318-1332
1558	PR00049D	Wilm's tumour protein signature IV	0.00 5.73e-09 259-273
1558	PR00554B	Adenosine A2B receptor signature II	12.52 8.85e-09 917-925
1558	PR00834F	HtrA/DegQ protease family signature VI	11.11 5.24e-09 194-206
1559	IPB000095F	PAK-box /P21-Rho-binding	16.47 4.51e-17 374-428
1559	IPB000861D	PKN/rhopilin/rhotekin rho-binding repeat	13.61 6.28e-09 148-184
1559	IPB000961A	Protein kinase C-terminal domain	16.82 4.60e-13 150-184
1559	IPB000961D	Protein kinase C-terminal domain	21.23 5.64e-09 366-407
1559	IPB001245B	Tyrosine kinase catalytic domain	21.68 2.38e-13 370-408
1559	IPB001772A	Kinase associated domain 1	13.64 7.21e-10 148-179
1559	IPB003527A	MAP kinase	17.00 3.49e-09 157-182
1560	IPB003104B	Formin Homology 2 Domain	18.83 6.87e-21 785-814
1560	IPB003104C	Formin Homology 2 Domain	20.33 1.27e-14 957-984
1565	IPB000590A	Hydroxymethylglutaryl-coenzyme A synthase	17.12 1.00e-28 50-74
1565	IPB000590B	Hydroxymethylglutaryl-coenzyme A synthase	16.61 1.67e-37 75-109
1565	IPB000590C	Hydroxymethylglutaryl-coenzyme A synthase	17.39 1.00e-40 110-156
1565	IPB000590D	Hydroxymethylglutaryl-coenzyme A synthase	13.35 5.50e-21 165-196
1565	IPB000590E	Hydroxymethylglutaryl-coenzyme A synthase	20.64 3.08e-31 306-359
1565	IPB000590F	Hydroxymethylglutaryl-coenzyme A synthase	16.80 4.27e-32 384-412
1565	IPB000590G	Hydroxymethylglutaryl-coenzyme A synthase	30.71 1.00e-40 448-502
1568	IPB003016	2-oxo acid dehydrogenases acyltransferase component lipoyl binding site	20.69 2.17e-20 103-137
1572	IPB002043C	Uracil-DNA glycosylase	14.49 2.24e-09 666-676
1574	IPB000637A	HMG-I and HMG-Y DNA-binding domain (A+T-hook)	12.35 7.32e-10 275-295
1574	IPB000840C	Matrix protein (MA)	15.25 8.46e-09 245-290
1574	IPB000949H	ELM2 domain	21.43 9.41e-09 218-264
1574	PR00049D	Wilm's tumour protein signature IV	0.00 4.66e-09 254-268
1574	PR00456E	Ribosomal protein P2 signature V	3.08 5.60e-09 184-198
1575	IPB002567G	Cell fusion glycoprotein K	17.37 9.32e-09 231-270
1577	PR00756B	Membrane alanyl dipeptidase (M1) family signature II	15.53 3.70e-13 232-247

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SEQ ID NO:	Database entry ID	Description	Results*
1577	PR00756C	Membrane alanyl dipeptidase (M1) family signature III	11.52 1.84e-11 310-320
1579	IPB000221	Protamine P1	5.48 8.01e-11 630-656
1579	IPB000221	Protamine P1	5.48 8.50e-09 626-652
1579	IPB000221	Protamine P1	5.48 9.65e-09 640-666
1579	IPB000492B	Protamine 2 (PRM2)	5.26 5.70e-09 662-696
1579	IPB000492B	Protamine 2 (PRM2)	5.26 7.36e-09 623-657
1579	IPB000822	Zinc finger, C2H2 type	14.67 7.38e-09 586-611
1579	IPB003868A	Herpesvirus UL31-like protein	9.31 6.11e-09 640-654
1580	IPB000215A	Serpins	13.01 5.91e-17 63-86
1580	IPB000215B	Serpins	9.87 2.29e-09 166-178
1580	IPB000215C	Serpins	13.90 4.32e-14 196-210
1580	IPB000215D	Serpins	15.35 4.41e-14 407-433
1581	IPB000557B	Calponin family repeat	17.28 1.63e-11 110-129
1581	IPB001715A	Calponin homology (CH) domain	10.74 7.86e-09 114-124
1581	PR00888C	Smooth muscle protein/calponin family signature III	11.52 9.86e-10 110-125
1581	PR00889B	Calponin signature II	9.54 9.00e-09 121-138
1582	IPB000483	Leucine rich repeat C-terminal domain	11.18 4.54e-10 369-383
1582	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 3.35e-11 475-512
1582	PR00019A	Leucine-rich repeat signature I	11.72 2.09e-09 95-108
1582	PR00019B	Leucine-rich repeat signature II	11.42 3.00e-10 140-153
1582	PR00019B	Leucine-rich repeat signature II	11.42 5.67e-10 92-105
1582	PR00019B	Leucine-rich repeat signature II	11.42 6.45e-09 116-129
1582	PR00019B	Leucine-rich repeat signature II	11.42 9.18e-09 164-177
1586	PR01256B	Otx1 transcription factor signature II	5.92 7.57e-09 33-45
1587	IPB001841	RING finger	10.69 1.00e-09 186-195
1587	IPB002867B	Cysteine-rich domain (C6HC)	22.50 4.15e-15 185-204
1590	IPB002889B	WSC domain	11.76 8.88e-09 98-144
1590	IPB002889B	WSC domain	11.76 9.70e-10 100-146
1592	IPB003888E	FY-rich domain N-terminus	19.80 9.00e-10 661-710
1593	IPB000103A	Pyridine nucleotide-disulphide oxidoreductase class-II	11.55 6.09e-10 747-767
1593	IPB000885A	Fibrillar collagen C-terminal domain	11.46 2.17e-10 481-518
1593	IPB000885A	Fibrillar collagen C-terminal domain	11.46 6.14e-09 475-512
1593	IPB000885B	Fibrillar collagen C-terminal domain	19.15 7.30e-09 609-662
1593	IPB000885B	Fibrillar collagen C-terminal domain	19.15 9.57e-10 320-373
1593	IPB001073A	Complement C1q protein	22.14 4.20e-10 483-517
1593	IPB001073A	Complement C1q protein	22.14 5.50e-09 486-520
1593	IPB001073A	Complement C1q protein	22.14 6.48e-09 342-376
1593	IPB001073A	Complement C1q protein	22.14 7.19e-09 726-760
1593	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 1.00e-08 480-532
1593	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 3.43e-09 468-520
1593	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 4.68e-09 613-665
1593	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 5.21e-10 462-514
1593	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 6.17e-09 483-535
1593	IPB001442A	C-terminal tandem repeated domain in type 4 procollagen	26.12 7.81e-09 459-511

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SEQ ID NO:	Database entry ID	Description	Results*
1593	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 2.34e-09 487-507
1593	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 6.11e-09 481-501
1593	IPB001442B	C-terminal tandem repeated domain in type 4 procollagen	12.38 7.69e-09 484-504
1593	IPB001451	Bacterial transferase hexapeptide repeat	18.07 2.15e-09 544-579
1593	IPB001451	Bacterial transferase hexapeptide repeat	18.07 5.14e-10 550-585
1593	IPB001451	Bacterial transferase hexapeptide repeat	18.07 8.20e-10 556-591
1593	IPB003474A	GntP family permease	20.01 7.98e-09 179-219
1593	PR00308A	Type I antifreeze protein signature I	3.72 1.00e-08 527-541
1593	PR00308A	Type I antifreeze protein signature I	3.72 3.77e-09 371-385
1593	PR00308A	Type I antifreeze protein signature I	3.72 6.13e-10 372-386
1593	PR00308A	Type I antifreeze protein signature I	3.72 9.31e-09 756-770
1593	PR00308A	Type I antifreeze protein signature I	3.72 9.48e-10 752-766
1593	PR00308C	Type I antifreeze protein signature III	2.79 2.30e-09 375-384
1593	PR00308C	Type I antifreeze protein signature III	2.79 8.82e-09 324-333
1593	PR00308C	Type I antifreeze protein signature III	2.79 9.53e-09 372-381
1593	PR00308C	Type I antifreeze protein signature III	2.79 9.59e-10 373-382
1593	PR00350E	Vitamin D receptor (II nuclear receptor) signature V	11.57 4.21e-09 13-32
1593	PR01286E	Orphan nuclear receptor NOR1 signature V	5.27 9.02e-09 365-386
1593	PR01500B	Tropoelastin signature II	7.08 1.20e-26 229-249
1593	PR01500C	Tropoelastin signature III	6.02 1.31e-24 306-324
1593	PR01511D	Kv1.4 voltage-gated K ⁺ channel signature IV	3.91 3.47e-09 373-383
1593	PR01511D	Kv1.4 voltage-gated K ⁺ channel signature IV	3.91 5.85e-09 326-336
1593	PR01511D	Kv1.4 voltage-gated K ⁺ channel signature IV	3.91 5.85e-09 757-767
1595	IPB000130	Neutral zinc metallopeptidases, zinc-binding region	5.86 5.71e-09 187-197
1595	PR00756C	Membrane alanyl dipeptidase (M1) family signature III	11.52 4.81e-12 151-161
1595	PR00756D	Membrane alanyl dipeptidase (M1) family signature IV	10.78 8.65e-19 187-202
1595	PR00756E	Membrane alanyl dipeptidase (M1) family signature V	10.37 2.42e-15 206-218
1600	IPB000716D	Thyroglobulin type-1 repeat	15.49 7.67e-13 96-110
1601	PR00342A	Rhesus blood group protein signature I	13.65 4.75e-21 12-30
1606	IPB002219B	Phorbol esters/diacylglycerol binding domain	12.53 9.13e-09 230-245
1606	IPB002857A	CXXC zinc finger	14.69 4.88e-21 68-99
1606	IPB002999C	Tudor domain	10.33 9.18e-09 540-549
1606	IPB003649B	B-Box C-terminal domain	22.16 7.57e-10 58-77
1606	PR00364D	Disease resistance protein signature IV	14.89 1.00e-08 730-746
1613	IPB002004A	Poly-adenylate binding protein, unique domain	18.93 5.36e-10 150-197
1614	PR00258B	Speract receptor signature II	7.94 7.75e-13 64-75
1614	PR00258C	Speract receptor signature III	9.05 2.72e-09 79-89
1614	PR00258D	Speract receptor signature IV	14.29 6.47e-10 110-124
1614	PR00258E	Speract receptor signature V	14.06 8.78e-13 133-145
1615	IPB003780E	Cytochrome oxidase assembly	15.53 7.40e-14 59-83
1616	IPB000135D	High mobility group proteins HMG1 and	2.13 1.00e-12 318-342

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SEQ ID NO:	Database entry ID	Description	Results*
		HMG2	
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 1.10e-10 317-341
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 2.16e-15 322-346
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 3.35e-11 327-351
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 3.82e-09 313-337
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 4.18e-09 316-340
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 4.47e-12 319-343
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 4.53e-14 320-344
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 4.58e-11 328-352
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 4.58e-12 326-350
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 5.11e-15 324-348
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 7.00e-09 330-354
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 7.69e-14 325-349
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 7.85e-10 329-353
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 8.12e-16 323-347
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 8.91e-09 315-339
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 9.80e-10 312-336
1616	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 9.87e-15 321-345
1616	IPB000533E	Tropomyosin	11.32 5.16e-09 380-417
1616	IPB000637B	HMG-I and HMG-Y DNA-binding domain (A+T-hook)	14.21 3.45e-09 324-342
1616	IPB000637B	HMG-I and HMG-Y DNA-binding domain (A+T-hook)	14.21 9.18e-09 328-346
1616	IPB001422C	Neuromodulin (GAP-43)	16.82 1.34e-09 322-357
1616	IPB001422C	Neuromodulin (GAP-43)	16.82 2.01e-09 318-353
1616	IPB001422C	Neuromodulin (GAP-43)	16.82 2.80e-09 320-355
1616	IPB001422C	Neuromodulin (GAP-43)	16.82 3.36e-09 321-356
1616	IPB001422C	Neuromodulin (GAP-43)	16.82 4.67e-10 323-358
1616	IPB001422C	Neuromodulin (GAP-43)	16.82 5.86e-10 324-359
1616	IPB001422C	Neuromodulin (GAP-43)	16.82 7.33e-13 319-354
1616	IPB001422C	Neuromodulin (GAP-43)	16.82 7.63e-10 317-352
1616	IPB001422C	Neuromodulin (GAP-43)	16.82 7.64e-09 315-350
1616	IPB001422C	Neuromodulin (GAP-43)	16.82 9.29e-10 314-349
1616	IPB001580F	Calreticulin family	2.93 4.94e-10 325-334
1616	IPB001580F	Calreticulin family	2.93 4.94e-10 326-335
1616	IPB001580F	Calreticulin family	2.93 4.94e-10 327-336
1616	IPB001580F	Calreticulin family	2.93 4.94e-10 328-337

Table 3B

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SEQ ID NO:	Database entry ID	Description	Results*
1616	IPB001580F	Calreticulin family	2.93 6.85e-09 331-340
1616	IPB001580F	Calreticulin family	2.93 7.75e-10 336-345
1616	IPB001990C	Granins (chromogranin or secretogranin)	33.59 8.59e-09 309-356
1616	IPB002172	Low density lipoprotein (LDL)-receptor class A (LDLRA) domain	7.37 2.96e-11 52-64
1616	IPB002172	Low density lipoprotein (LDL)-receptor class A (LDLRA) domain	7.37 8.20e-12 93-105
1616	IPB002360C	Involucrin	15.36 9.80e-09 327-368
1616	PR00194D	Tropomyosin signature IV	9.54 8.25e-09 323-346
1616	PR00261A	Low density lipoprotein (LDL) receptor signature I	15.49 4.19e-10 43-64
1616	PR00261A	Low density lipoprotein (LDL) receptor signature I	15.49 4.60e-09 84-105
1616	PR00261B	Low density lipoprotein (LDL) receptor signature II	15.12 2.80e-10 84-105
1616	PR00261B	Low density lipoprotein (LDL) receptor signature II	15.12 6.03e-09 43-64
1616	PR00261C	Low density lipoprotein (LDL) receptor signature III	18.72 3.03e-09 43-64
1616	PR00261D	Low density lipoprotein (LDL) receptor signature IV	16.87 4.25e-10 84-105
1616	PR00261D	Low density lipoprotein (LDL) receptor signature IV	16.87 8.45e-11 43-64
1616	PR00261E	Low density lipoprotein (LDL) receptor signature V	18.62 7.52e-09 84-105
1616	PR00261E	Low density lipoprotein (LDL) receptor signature V	18.62 7.83e-09 43-64
1616	PR00261F	Low density lipoprotein (LDL) receptor signature VI	15.46 2.65e-11 43-64
1616	PR00261F	Low density lipoprotein (LDL) receptor signature VI	15.46 6.91e-10 84-105
1617	IPB002554A	Protein phosphatase 2A regulatory B subunit (B56 family)	19.95 2.29e-27 165-194
1618	IPB003029B	S1 RNA binding domain	9.42 8.80e-09 407-418
1619	IPB000001D	Kringle	11.31 2.88e-12 55-71
1619	IPB000126A	Serine proteases, V8 family	11.75 6.60e-09 55-70
1619	IPB001254A	Serine proteases, trypsin family	9.98 7.65e-14 55-71
1619	PR00722A	Chymotrypsin serine protease family (S1) signature I	12.06 9.36e-14 56-71
1619	PR00839B	V8 serine protease family signature II	11.20 4.95e-09 55-72
1620	IPB000934C	Serine/threonine specific protein phosphatase	20.25 3.00e-34 71-114
1620	IPB000934D	Serine/threonine specific protein phosphatase	14.86 9.55e-17 116-135
1620	IPB000934E	Serine/threonine specific protein phosphatase	25.16 2.88e-27 180-223
1620	PR00114D	Serine/threonine phosphatase family signature IV	11.97 4.60e-24 77-103
1620	PR00114E	Serine/threonine phosphatase family signature V	17.50 7.63e-23 106-133
1620	PR00114F	Serine/threonine phosphatase family signature VI	16.38 2.93e-15 170-190
1620	PR00114G	Serine/threonine phosphatase family signature VII	15.51 9.57e-17 198-214

Table 3B
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SEQ ID NO:	Database entry ID	Description	Results*
1623	PR01008D	Flagellar L-ring protein signature IV	9.99 8.13e-17 35-49
1623	PR01008E	Flagellar L-ring protein signature V	13.32 6.48e-17 51-65
1623	PR01010G	Flagellar P-ring protein signature VII	12.40 8.11e-20 88-106
1623	PR01010H	Flagellar P-ring protein signature VIII	12.18 8.88e-18 114-132
1623	PR01010I	Flagellar P-ring protein signature IX	7.74 8.11e-11 178-190
1624	IPB002195C	Dihydroorotase	11.49 8.26e-12 98-109
1624	IPB002604F	Chlorohydrolase	11.98 3.86e-09 130-139
1624	IPB003764D	N-acetylglucosamine-6-phosphate deacetylase	33.54 8.05e-09 114-156
1625	IPB000319C	Aspartate-semialdehyde dehydrogenase	12.28 6.63e-10 61-77
1625	IPB000319D	Aspartate-semialdehyde dehydrogenase	13.92 8.90e-16 91-112
1625	IPB000319E	Aspartate-semialdehyde dehydrogenase	5.68 3.68e-09 155-165
1625	IPB000319F	Aspartate-semialdehyde dehydrogenase	12.86 4.96e-10 238-251
1625	IPB000319G	Aspartate-semialdehyde dehydrogenase	14.74 9.79e-16 258-278
1625	IPB000534A	Semialdehyde dehydrogenase	15.79 7.88e-11 64-81
1628	IPB000847	Bacterial regulatory protein, LysR family	15.44 8.67e-15 21-54
1628	IPB001804D	Isocitrate and isopropylmalate dehydrogenases	24.39 9.18e-09 208-235
1631	IPB000121C	PEP-utilizing enzyme	12.96 5.15e-15 96-108
1631	IPB002192G	Pyruvate phosphate dikinase, PEP/pyruvate binding domain	23.23 3.77e-16 78-109
1631	PR00811C	Bacterial general secretion pathway protein D signature III	10.47 6.20e-09 9-19
1632	IPB002029C	Aspartate and ornithine carbamoyltransferase family	27.21 8.14e-21 401-439
1632	IPB003462C	Ornithine cyclodeaminase/mu-crystallin family	8.98 7.00e-09 500-513
1632	PR00101C	Aspartate carbamoyltransferase signature III	15.49 8.93e-10 410-427
1632	PR01375B	Salmonella/Shigella invasin protein B signature II	7.54 9.67e-09 201-217
1632	PR01507H	Melanin-concentrating hormone 1 receptor signature VIII	11.93 6.53e-09 354-373
1634	IPB001568B	Ribonuclease T2 family	11.65 1.00e-17 101-112
1643	IPB001014	Ribosomal L23 protein	22.21 6.03e-20 217-249
1645	PR01303D	Plasmodium circumsporozoite protein signature IV	10.57 6.88e-09 486-503
1647	IPB001518B	Argininosuccinate synthase	12.16 6.87e-12 58-70
1647	IPB001518C	Argininosuccinate synthase	27.71 3.57e-27 72-114
1647	IPB001518E	Argininosuccinate synthase	20.16 5.24e-14 172-188
1651	PR00453A	Von Willebrand factor type A domain signature I	11.78 3.89e-13 88-105
1651	PR00453B	Von Willebrand factor type A domain signature II	13.84 6.10e-13 125-139
1651	PR00453C	Von Willebrand factor type A domain signature III	11.84 3.57e-10 246-254
1654	IPB000222B	Protein phosphatase 2C subfamily	15.80 6.66e-09 94-104
1654	IPB000222C	Protein phosphatase 2C subfamily	6.84 5.86e-11 118-127
1657	IPB000917A	Sulfatase	9.52 4.79e-10 47-58
1658	IPB000063	Thioredoxin	9.89 1.69e-16 346-359
1658	IPB000063	Thioredoxin	9.89 2.38e-16 481-494
1658	PR00421A	Thioredoxin family signature I	10.35 1.00e-10 481-489
1658	PR00421A	Thioredoxin family signature I	10.35 2.13e-11 346-354
1658	PR00421B	Thioredoxin family signature II	10.23 1.00e-11 354-363
1658	PR00421B	Thioredoxin family signature II	10.23 7.75e-12 489-498

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SEQ ID NO:	Database entry ID	Description	Results*
1658	PR00421C	Thioredoxin family signature III	11.02 1.00e-09 394-405
1658	PR00421C	Thioredoxin family signature III	11.02 3.84e-10 533-544
1661	IPB003134F	Repeat in HS1/Cortactin	15.66 9.68e-09 101-149
1662	IPB002360C	Involucrin	15.36 9.00e-09 56-97
1662	PR01270A	Histone deacetylase superfamily signature I	14.72 6.85e-10 1235-1258
1662	PR01270B	Histone deacetylase superfamily signature II	9.70 5.76e-18 1269-1284
1662	PR01270C	Histone deacetylase superfamily signature III	10.89 3.57e-09 1360-1370
1663	PR01104A	Anaphylatoxin chemotactic receptor signature I	13.83 8.50e-09 83-94
1666	IPB000737	Serine protease inhibitor, squash family	13.14 8.31e-14 85-104
1666	IPB002098	Seminal vesicle protein I repeats	9.00 1.00e-40 31-67
1666	IPB002098	Seminal vesicle protein I repeats	9.00 1.43e-16 43-79
1666	IPB002098	Seminal vesicle protein I repeats	9.00 2.54e-17 19-55
1666	IPB002098	Seminal vesicle protein I repeats	9.00 3.79e-15 37-73
1666	IPB002098	Seminal vesicle protein I repeats	9.00 7.15e-18 25-61
1666	IPB002098	Seminal vesicle protein I repeats	9.00 9.83e-10 49-85
1666	IPB002221B	WAP-type (Whey Acidic Protein) four-disulfide core domain	17.12 3.14e-20 92-113
1666	PR00003A	4-disulphide core signature I	14.31 7.00e-09 69-78
1666	PR00003C	4-disulphide core signature III	7.81 7.63e-12 98-107
1666	PR00003D	4-disulphide core signature IV	9.63 8.50e-09 108-116
1667	IPB001909	KRAB box	17.37 1.00e-32 108-142
1673	IPB003150C	RFX DNA-binding domain	25.34 7.08e-09 248-294
1674	IPB001322A	Intermediate filament tail domain	30.52 7.88e-11 63-116
1674	PR01002A	Flagellar protein FlgJ signature I	10.02 9.65e-09 261-281
1676	IPB001865A	Ribosomal protein S2	35.08 8.94e-11 53-106
1678	PR00795C	Ryanodine receptor signature III	6.10 7.92e-09 107-131
1684	IPB001998A	Xylose isomerase	15.52 3.05e-09 214-227
1684	IPB002198	Short-chain dehydrogenase/reductase (SDR) superfamily	19.72 8.80e-20 133-168
1684	PR00080C	Short-chain dehydrogenase/reductase (SDR) superfamily signature III	14.49 8.83e-13 153-172
1684	PR00081A	Glucose/ribitol dehydrogenase family signature I	10.07 8.20e-10 5-22
1684	PR00081C	Glucose/ribitol dehydrogenase family signature III	12.71 7.97e-09 127-143
1684	PR00081D	Glucose/ribitol dehydrogenase family signature IV	15.22 4.71e-10 153-172
1684	PR01167F	Insect alcohol dehydrogenase family signature VI	11.22 2.34e-09 152-170
1685	IPB001526C	Ly-6/u-PAR domain	13.04 2.03e-09 197-212
1685	PR01514F	Kv2.1 voltage-gated K ⁺ channel signature VI	2.00 5.29e-09 220-231
1686	IPB000095E	PAK-box /P21-Rho-binding	17.62 7.35e-13 679-724
1686	IPB000961C	Protein kinase C-terminal domain	15.48 5.50e-12 678-712
1686	IPB001245A	Tyrosine kinase catalytic domain	22.45 8.88e-16 671-711
1686	IPB001245B	Tyrosine kinase catalytic domain	21.68 8.64e-09 736-774
1686	IPB003527C	MAP kinase	14.70 5.30e-09 663-711
1686	IPB003605C	GS motif preceding kinase domain in TGF beta receptor	14.92 2.91e-15 570-617
1686	IPB003605D	GS motif preceding kinase domain in TGF beta receptor	12.41 4.39e-16 667-708

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SEQ ID NO:	Database entry ID	Description	Results*
1686	IPB003605E	GS motif preceding kinase domain in TGF beta receptor	21.14 3.61e-15 710-749
1686	IPB003605F	GS motif preceding kinase domain in TGF beta receptor	23.21 2.56e-12 826-879
1686	PR00653D	Activin type II receptor signature IV	12.01 9.76e-12 697-718
1686	PR00653E	Activin type II receptor signature V	14.33 2.93e-16 871-890
1687	IPB000832A	G-protein coupled receptors family 2 (secretin-like)	13.81 3.25e-13 94-109
1687	PR00491A	Vasoactive intestinal peptide receptor signature I	12.62 2.98e-09 109-120
1687	PR01154A	Vasoactive intestinal peptide receptor 1 signature I	11.05 3.84e-29 58-79
1687	PR01154B	Vasoactive intestinal peptide receptor 1 signature II	12.24 1.39e-22 95-111
1688	PR00401A	SH2 domain signature I	12.88 6.29e-15 214-228
1688	PR00452A	SH3 domain signature I	9.57 2.35e-10 150-160
1688	PR00452B	SH3 domain signature II	11.47 4.91e-12 164-179
1688	PR00452C	SH3 domain signature III	10.63 4.60e-09 181-190
1688	PR00499D	Neutrophil cytosol factor 2 signature IV	11.47 8.29e-10 152-172
1688	PR01260A	Na ⁺ /Ca ²⁺ exchanger isoform 1 signature I	9.46 2.75e-09 5-17
1693	PR00019A	Leucine-rich repeat signature I	11.72 1.27e-09 660-673
1693	PR00019A	Leucine-rich repeat signature I	11.72 1.55e-09 614-627
1693	PR00019B	Leucine-rich repeat signature II	11.42 7.55e-11 527-540
1693	PR00019B	Leucine-rich repeat signature II	11.42 8.91e-09 611-624
1694	PR00499B	Neutrophil cytosol factor 2 signature II	9.48 4.73e-09 34-53
1695	IPB001359H	Synapsin	22.58 4.58e-09 150-200
1704	IPB000272	ATP1G1/PLM/MAT8 family	14.36 8.53e-09 28-63
1705	IPB000892B	Ribosomal protein S26E	13.49 3.50e-27 160-196
1706	IPB000906D	ZU5 domain	23.89 2.54e-09 368-422
1706	IPB000906D	ZU5 domain	23.89 5.71e-09 437-491
1706	IPB000906D	ZU5 domain	23.89 8.54e-09 401-455
1706	IPB000906E	ZU5 domain	22.11 1.38e-09 448-488
1706	IPB000906G	ZU5 domain	25.85 3.64e-10 382-430
1706	IPB000906G	ZU5 domain	25.85 5.87e-09 451-499
1706	IPB001580F	Calreticulin family	2.93 8.20e-09 317-326
1706	IPB003716C	RNA polymerase omega subunit	13.72 9.39e-09 314-334
1706	PR00019B	Leucine-rich repeat signature II	11.42 1.55e-09 742-755
1706	PR00019B	Leucine-rich repeat signature II	11.42 5.67e-10 773-786
1706	PR01415A	Ankyrin repeat signature I	12.73 1.45e-13 415-427
1706	PR01415A	Ankyrin repeat signature I	12.73 4.19e-10 451-463
1706	PR01415B	Ankyrin repeat signature II	10.23 1.90e-10 463-475
1706	PR01415B	Ankyrin repeat signature II	10.23 2.93e-12 427-439
1708	IPB000822	Zinc finger, C2H2 type	14.67 1.00e-18 235-260
1708	IPB000822	Zinc finger, C2H2 type	14.67 2.93e-17 207-232
1708	IPB000822	Zinc finger, C2H2 type	14.67 6.57e-10 263-288
1708	IPB000822	Zinc finger, C2H2 type	14.67 8.71e-10 53-78
1708	IPB001275	DM DNA binding domain	19.17 7.04e-09 223-262
1708	PR00048A	C2H2-type zinc finger signature I	9.94 1.00e-08 204-217
1708	PR00048A	C2H2-type zinc finger signature I	9.94 4.38e-09 232-245
1708	PR00048A	C2H2-type zinc finger signature I	9.94 7.00e-09 260-273
1708	PR00048A	C2H2-type zinc finger signature I	9.94 9.63e-09 50-63
1708	PR00048B	C2H2-type zinc finger signature II	5.52 7.43e-10 220-229
1708	PR00498A	Neutrophil cytosol factor 1 signature I	12.92 6.74e-09 353-361
1709	IPB002870A	Reprolysin family propeptide	12.22 4.09e-10 108-124

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SEQ ID NO:	Database entry ID	Description	Results*
1710	IPB000222B	Protein phosphatase 2C subfamily	15.80 9.49e-09 1539-1549
1710	IPB001389D	Flocculin repeat	9.66 5.93e-09 1712-1739
1710	PR01391C	Binary toxin B family signature III	14.87 5.44e-09 259-277
1711	PR01099B	Hydroxyethylthiazole kinase family signature II	14.42 5.44e-09 6-27
1712	IPB000716C	Thyroglobulin type-1 repeat	17.62 5.41e-12 287-305
1712	IPB000867A	Insulin-like growth factor-binding protein	7.19 7.19e-09 48-55
1712	IPB000867B	Insulin-like growth factor-binding protein	11.44 4.13e-18 66-82
1712	PR01169I	Ceratitis capitata alcohol dehydrogenase signature IX	10.85 9.41e-09 425-445
1715	IPB003308C	Integrase zinc-binding domain	19.91 3.42e-33 22-75
1715	IPB003308D	Integrase zinc-binding domain	8.41 7.43e-09 94-106
1715	IPB003308E	Integrase zinc-binding domain	9.08 1.20e-11 166-179
1717	IPB001134C	Netrin, C-terminus	17.82 7.82e-10 1317-1331
1717	IPB001599A	Alpha-2-macroglobulin family	10.97 1.45e-21 175-193
1717	IPB001599B	Alpha-2-macroglobulin family	7.45 3.35e-14 264-276
1717	IPB001599C	Alpha-2-macroglobulin family	14.40 4.60e-15 291-307
1717	IPB001599D	Alpha-2-macroglobulin family	11.61 4.94e-15 783-793
1717	IPB001599E	Alpha-2-macroglobulin family	11.06 1.60e-10 810-819
1717	IPB001599F	Alpha-2-macroglobulin family	18.95 5.30e-27 840-869
1717	IPB001599G	Alpha-2-macroglobulin family	13.87 1.53e-13 988-997
1717	IPB001599H	Alpha-2-macroglobulin family	18.42 1.00e-23 1020-1047
1717	IPB001599I	Alpha-2-macroglobulin family	10.83 4.33e-12 1057-1066
1717	IPB001599J	Alpha-2-macroglobulin family	20.99 3.10e-16 1088-1113
1717	IPB001599K	Alpha-2-macroglobulin family	8.15 7.60e-13 1273-1284
1717	IPB001599L	Alpha-2-macroglobulin family	18.66 4.00e-25 1304-1331
1717	IPB001599M	Alpha-2-macroglobulin family	13.29 1.75e-12 1445-1456
1717	IPB001599N	Alpha-2-macroglobulin family	24.85 9.22e-26 1498-1530
1717	IPB001983D	Translationally controlled tumor protein	22.98 6.63e-13 1213-1253
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 1.00e-12 217-241
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 2.41e-15 219-243
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 2.86e-17 220-244
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 3.43e-14 218-242
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 4.58e-11 214-238
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 5.23e-12 223-247
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 5.60e-10 213-237
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 6.18e-09 212-236
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 7.56e-15 222-246
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 8.06e-11 224-248
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 8.30e-14 216-240
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 9.13e-12 215-239
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 9.14e-17 221-245

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SEQ ID NO:	Database entry ID	Description	Results*
		HMG2	
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 9.18e-11 225-249
1718	IPB000135D	High mobility group proteins HMG1 and HMG2	2.13 9.64e-09 226-250
1718	IPB000637B	HMG-I and HMG-Y DNA-binding domain (A+T-hook)	14.21 1.00e-08 224-242
1718	IPB000637B	HMG-I and HMG-Y DNA-binding domain (A+T-hook)	14.21 1.00e-08 225-243
1718	IPB000637B	HMG-I and HMG-Y DNA-binding domain (A+T-hook)	14.21 2.09e-09 223-241
1718	IPB000637B	HMG-I and HMG-Y DNA-binding domain (A+T-hook)	14.21 4.82e-09 221-239
1718	IPB000637B	HMG-I and HMG-Y DNA-binding domain (A+T-hook)	14.21 8.36e-09 222-240
1718	IPB001422C	Neuromodulin (GAP-43)	16.82 2.07e-10 218-253
1718	IPB001422C	Neuromodulin (GAP-43)	16.82 2.13e-09 222-257
1718	IPB001422C	Neuromodulin (GAP-43)	16.82 3.70e-09 220-255
1718	IPB001422C	Neuromodulin (GAP-43)	16.82 3.84e-10 217-252
1718	IPB001422C	Neuromodulin (GAP-43)	16.82 6.68e-10 223-258
1718	IPB001422C	Neuromodulin (GAP-43)	16.82 6.74e-09 221-256
1718	IPB001422C	Neuromodulin (GAP-43)	16.82 8.93e-10 225-260
1718	IPB001580F	Calreticulin family	2.93 4.94e-10 224-233
1718	IPB001580F	Calreticulin family	2.93 4.94e-10 225-234
1718	IPB001580F	Calreticulin family	2.93 4.94e-10 226-235
1718	IPB001580F	Calreticulin family	2.93 4.94e-10 227-236
1718	IPB001580F	Calreticulin family	2.93 4.94e-10 228-237
1718	IPB001580F	Calreticulin family	2.93 4.94e-10 229-238
1718	IPB001580F	Calreticulin family	2.93 4.94e-10 230-239
1718	IPB001580F	Calreticulin family	2.93 4.94e-10 231-240
1718	IPB001580F	Calreticulin family	2.93 4.94e-10 232-241
1718	IPB001580F	Calreticulin family	2.93 4.94e-10 233-242
1718	IPB001580F	Calreticulin family	2.93 4.94e-10 234-243
1718	IPB001580F	Calreticulin family	2.93 7.75e-09 235-244
1718	IPB002126A	Cadherin domain	14.68 7.00e-09 119-135
1718	IPB002126B	Cadherin domain	12.04 5.20e-16 422-439
1718	IPB002126B	Cadherin domain	12.04 7.86e-13 156-173
1718	IPB002126C	Cadherin domain	12.35 8.41e-09 398-408
1718	PR00194D	Tropomyosin signature IV	9.54 1.94e-09 222-245
1718	PR00194D	Tropomyosin signature IV	9.54 2.05e-09 220-243
1718	PR00205A	Cadherin signature I	17.38 3.50e-13 108-127
1718	PR00205B	Cadherin signature II	20.09 3.30e-11 551-580
1718	PR00205B	Cadherin signature II	20.09 4.66e-14 434-463
1718	PR00205B	Cadherin signature II	20.09 9.50e-21 168-197
1718	PR00205C	Cadherin signature III	13.59 3.25e-11 397-409
1718	PR00205D	Cadherin signature IV	12.22 4.46e-19 413-432
1718	PR00205E	Cadherin signature V	10.82 4.32e-11 432-445
1718	PR00205F	Cadherin signature VI	19.57 4.77e-10 380-406
1718	PR00205F	Cadherin signature VI	19.57 5.20e-13 493-519
1718	PR00205F	Cadherin signature VI	19.57 7.30e-13 115-141
1718	PR00205G	Cadherin signature VII	13.05 8.71e-14 416-433
1720	IPB003360A	US22-like viral protein	16.29 4.27e-09 133-146
1722	IPB001128	none	11.42 5.15e-13 469-481
1722	PR00385A	P450 superfamily signature I	13.94 4.19e-10 341-358

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SEQ ID NO:	Database entry ID	Description	Results*
1722	PR00385C	P450 superfamily signature III	17.08 6.29e-10 395-406
1722	PR00385D	P450 superfamily signature IV	11.11 9.47e-10 470-479
1722	PR00385E	P450 superfamily signature V	13.50 5.50e-09 479-490
1722	PR00463H	E-class P450 group I signature VIII	11.44 5.68e-10 469-479
1722	PR00465B	E-class P450 group IV signature II	17.22 7.92e-10 113-136
1722	PR00465C	E-class P450 group IV signature III	20.35 8.92e-23 332-358
1722	PR00465D	E-class P450 group IV signature IV	15.21 8.62e-16 390-406
1722	PR00465E	E-class P450 group IV signature V	15.83 4.41e-13 423-437
1722	PR00465F	E-class P450 group IV signature VI	13.57 1.00e-13 439-457
1722	PR00465G	E-class P450 group IV signature VII	15.73 8.07e-16 463-479
1722	PR00465H	E-class P450 group IV signature VIII	19.55 9.25e-21 479-497
1726	IPB003006A	Immunoglobulin and major histocompatibility complex domain	17.51 7.65e-12 91-113
1726	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 2.80e-10 130-167
1727	IPB001285A	Synaptophysin/synaptoporin	12.19 1.00e-40 26-72
1727	IPB001285B	Synaptophysin/synaptoporin	21.42 2.00e-35 73-104
1727	IPB001285B	Synaptophysin/synaptoporin	21.42 7.86e-12 72-103
1727	IPB001285C	Synaptophysin/synaptoporin	15.24 1.00e-40 108-148
1727	IPB001285D	Synaptophysin/synaptoporin	12.74 1.00e-40 149-183
1727	IPB001285E	Synaptophysin/synaptoporin	9.55 1.00e-40 184-230
1727	IPB001285F	Synaptophysin/synaptoporin	6.39 1.00e-40 231-275
1727	IPB001285F	Synaptophysin/synaptoporin	6.39 1.54e-09 248-292
1727	IPB001285F	Synaptophysin/synaptoporin	6.39 3.46e-09 242-286
1727	IPB001285F	Synaptophysin/synaptoporin	6.39 8.65e-11 258-302
1727	IPB001285F	Synaptophysin/synaptoporin	6.39 9.83e-11 263-307
1727	PR00220A	Synaptophysin/synaptoporin family signature I	13.69 1.41e-27 23-45
1727	PR00220B	Synaptophysin/synaptoporin family signature II	17.03 8.31e-28 47-72
1727	PR00220C	Synaptophysin/synaptoporin family signature III	11.86 7.00e-28 100-124
1727	PR00220D	Synaptophysin/synaptoporin family signature IV	10.60 8.13e-28 132-155
1727	PR00220E	Synaptophysin/synaptoporin family signature V	4.56 5.68e-23 199-217
1727	PR00761A	Bindin precursor signature I	6.20 7.00e-10 287-303
1728	IPB002360C	Involucrin	15.36 1.40e-09 114-155
1728	IPB002360C	Involucrin	15.36 7.80e-09 105-146
1728	IPB002558F	I/LWEQ domain	14.64 7.33e-09 155-185
1729	IPB003137	Protease associated (PA) domain	22.40 2.86e-15 551-581
1729	PR00747C	Glycosyl hydrolase family 47 signature III	12.34 5.14e-11 145-163
1729	PR00747E	Glycosyl hydrolase family 47 signature V	14.81 2.08e-18 225-242
1729	PR00747H	Glycosyl hydrolase family 47 signature VIII	12.76 5.50e-17 326-346
1730	PR00209C	Alpha/beta gliadin family signature III	3.37 5.39e-09 77-90
1731	IPB000276B	Rhodopsin-like GPCR superfamily	4.97 9.05e-09 192-203
1731	IPB000276C	Rhodopsin-like GPCR superfamily	8.03 3.50e-11 244-255
1731	IPB000276D	Rhodopsin-like GPCR superfamily	9.40 9.47e-14 285-301
1731	PR00237A	Rhodopsin-like GPCR superfamily signature I	9.81 2.42e-13 35-59
1731	PR00237B	Rhodopsin-like GPCR superfamily signature II	12.45 5.24e-16 68-89
1731	PR00237D	Rhodopsin-like GPCR superfamily signature IV	9.76 1.47e-11 133-154

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SEQ ID NO:	Database entry ID	Description	Results*
1731	PR00237E	Rhodopsin-like GPCR superfamily signature V	13.03 8.07e-11 184-207
1731	PR00237F	Rhodopsin-like GPCR superfamily signature VI	14.34 2.89e-17 234-258
1731	PR00237G	Rhodopsin-like GPCR superfamily signature VII	19.23 8.11e-19 275-301
1731	PR00244A	Neurokinin receptor signature I	10.06 5.00e-15 29-40
1731	PR00244B	Neurokinin receptor signature II	12.18 1.00e-13 55-64
1731	PR00244C	Neurokinin receptor signature III	13.48 2.87e-12 108-118
1731	PR00244D	Neurokinin receptor signature IV	7.47 9.36e-14 125-135
1731	PR00244E	Neurokinin receptor signature V	5.67 1.44e-11 183-192
1731	PR00244F	Neurokinin receptor signature VI	12.03 6.29e-16 204-217
1731	PR00244G	Neurokinin receptor signature VII	9.65 1.45e-15 268-279
1731	PR00244H	Neurokinin receptor signature VIII	13.18 5.50e-26 294-312
1731	PR01025A	Neurokinin NK2 receptor signature I	8.63 5.50e-16 2-15
1731	PR01025B	Neurokinin NK2 receptor signature II	12.20 7.11e-17 15-28
1731	PR01025C	Neurokinin NK2 receptor signature III	18.53 2.23e-16 154-166
1731	PR01025D	Neurokinin NK2 receptor signature IV	12.91 5.60e-18 168-182
1731	PR01025E	Neurokinin NK2 receptor signature V	8.25 7.23e-25 212-230
1731	PR01025F	Neurokinin NK2 receptor signature VI	14.52 1.00e-17 257-269
1731	PR01025G	Neurokinin NK2 receptor signature VII	9.85 6.65e-23 312-331
1733	IPB000917A	Sulfatase	9.52 5.26e-10 44-55
1734	PR00464A	Group II E-class P450 signature I	19.27 7.26e-14 167-187
1735	IPB000237B	GRIP domain	30.66 8.14e-09 273-323
1735	IPB002097C	Profilin	22.96 4.04e-10 986-1040
1735	IPB002097C	Profilin	22.96 5.08e-09 991-1045
1735	IPB003753G	Exonuclease VII, large subunit	31.72 8.85e-09 787-831
1735	PR00392C	Profilin signature III	14.42 2.29e-09 986-1006
1735	PR00392D	Profilin signature IV	10.64 4.35e-09 1008-1022
1738	IPB001138	Fungal transcriptional regulatory protein, N-terminus	12.17 9.79e-09 62-78
1739	IPB001509A	NAD dependent epimerase/dehydratase family	14.43 9.65e-09 379-400
1741	IPB003644J	Domain found in Na-Ca exchanger and integrin-beta4	13.64 5.67e-09 57-111
1741	PR00915G	Luteovirus group 1 coat protein signature VII	15.74 6.58e-10 303-324
1745	IPB001283A	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	16.26 6.67e-10 29-48
1745	IPB001283B	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	13.09 2.33e-12 57-72
1745	IPB001283E	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	13.34 5.50e-20 127-147
1745	IPB003106E	Homeobox associated leucine zipper	13.73 6.90e-09 25-55
1745	PR00837A	Allergen V5/Tpx-1 family signature I	14.69 1.56e-14 57-75
1745	PR00837C	Allergen V5/Tpx-1 family signature III	16.31 5.50e-20 126-142
1745	PR00838D	Venom allergen 5 signature IV	8.59 3.57e-09 57-75
1745	PR00838G	Venom allergen 5 signature VII	15.39 8.60e-18 125-144
1749	PR00672D	Inhibin beta C chain signature IV	10.52 6.40e-09 96-112
1749	PR01035I	Tetracycline resistance protein signature IX	13.24 3.86e-09 568-589
1749	PR01221G	Rodent urinary protein signature VII	12.11 8.68e-10 61-78
1750	IPB000885A	Fibrillar collagen C-terminal domain	11.46 8.16e-09 1852-1889
1751	IPB001991A	Sodium:dicarboxylate symporter family	10.78 2.53e-20 9-40
1751	IPB001991B	Sodium:dicarboxylate symporter family	14.40 2.29e-33 324-355

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SEQ ID NO:	Database entry ID	Description	Results*
1751	IPB001991C	Sodium:dicarboxylate symporter family	9.91 3.40e-24 375-394
1751	PR00173B	Glutamate-aspartate symporter signature II	7.82 7.87e-12 19-39
1751	PR00173C	Glutamate-aspartate symporter signature III	10.67 9.44e-26 327-352
1753	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 6.54e-09 286-323
1755	IPB002617C	Vesicular monoamine transporter	16.23 5.03e-10 91-143
1755	PR01035E	Tetracycline resistance protein signature V	10.87 2.08e-09 101-123
1755	PR01035F	Tetracycline resistance protein signature VI	12.88 7.52e-09 332-352
1757	IPB000300B	Inositol polyphosphate related phosphatase family	15.64 1.93e-16 468-491
1757	IPB000300C	Inositol polyphosphate related phosphatase family	14.50 8.50e-12 538-548
1757	IPB000300D	Inositol polyphosphate related phosphatase family	29.87 4.51e-18 589-623
1757	IPB000300E	Inositol polyphosphate related phosphatase family	15.50 1.43e-14 774-790
1757	IPB000492B	Protamine 2 (PRM2)	5.26 4.23e-09 83-117
1758	PR00169B	Potassium channel signature II	16.49 8.80e-28 239-267
1758	PR00169C	Potassium channel signature III	17.53 9.83e-11 307-330
1758	PR01496C	Shaker voltage-gated K ⁺ channel family signature III	9.37 6.92e-12 202-213
1758	PR01496D	Shaker voltage-gated K ⁺ channel family signature IV	9.74 3.25e-21 236-252
1758	PR01496E	Shaker voltage-gated K ⁺ channel family signature V	10.86 2.11e-14 259-270
1758	PR01509A	Kv1.2 voltage-gated K ⁺ channel signature I	6.59 3.57e-17 278-292
1758	PR01509B	Kv1.2 voltage-gated K ⁺ channel signature II	8.19 1.26e-17 294-306
1759	IPB000631B	Uncharacterized protein family UPF0031	10.96 5.00e-12 100-112
1759	IPB000631C	Uncharacterized protein family UPF0031	12.87 7.75e-12 376-387
1759	IPB000631E	Uncharacterized protein family UPF0031	7.82 9.25e-11 458-468
1762	IPB001734A	Sodium:solute symporter family	14.69 8.83e-13 40-56
1762	IPB001734B	Sodium:solute symporter family	18.26 5.50e-26 155-195
1762	IPB001734C	Sodium:solute symporter family	18.21 2.16e-21 448-477
1763	IPB000483	Leucine rich repeat C-terminal domain	11.18 2.23e-12 358-372
1763	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 5.15e-09 462-499
1763	PR00019A	Leucine-rich repeat signature I	11.72 5.50e-12 86-99
1763	PR00019A	Leucine-rich repeat signature I	11.72 8.91e-09 278-291
1763	PR00019B	Leucine-rich repeat signature II	11.42 1.00e-08 107-120
1763	PR00019B	Leucine-rich repeat signature II	11.42 8.77e-11 83-96
1763	PR00019B	Leucine-rich repeat signature II	11.42 9.67e-10 275-288
1764	IPB000130	Neutral zinc metallopeptidases, zinc-binding region	5.86 6.57e-09 294-304
1764	IPB001762A	Disintegrin	23.93 5.21e-10 241-281
1764	IPB001862A	Membrane attack complex components/perforin/complement C9	12.54 1.76e-10 416-431
1764	IPB002861B	Reeler domain	10.50 1.41e-09 422-450
1764	IPB002870D	Reprolysin family propeptide	16.31 6.25e-12 265-280
1764	IPB002870E	Reprolysin family propeptide	11.90 4.41e-12 296-308
1764	IPB002870F	Reprolysin family propeptide	18.81 3.73e-13 335-359
1764	PR00977A	Scytalidopepsin B aspartic protease (A4) signature I	7.30 9.11e-09 233-255
1765	PR00824A	Hepatic lipase signature I	8.11 4.44e-22 6-24

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SEQ ID NO:	Database entry ID	Description	Results*
1768	IPB000337A	G-protein coupled receptors family 3 (Metabotropic glutamate receptor-like)	9.17 4.32e-14 47-58
1768	IPB000337B	G-protein coupled receptors family 3 (Metabotropic glutamate receptor-like)	24.51 9.90e-09 150-198
1768	IPB001828A	Receptor family ligand binding region	13.21 9.05e-09 74-86
1768	PR00248A	Metabotropic glutamate GPCR signature I	7.46 9.10e-16 46-58
1768	PR00248B	Metabotropic glutamate GPCR signature II	12.69 2.89e-17 75-90
1768	PR00248C	Metabotropic glutamate GPCR signature III	11.96 8.20e-24 90-109
1768	PR00248D	Metabotropic glutamate GPCR signature IV	14.23 9.00e-15 153-179
1768	PR01054A	Metabotropic glutamate receptor 4 signature I	7.72 1.22e-25 9-26
1768	PR01054B	Metabotropic glutamate receptor 4 signature II	9.34 1.47e-26 26-44
1768	PR01054C	Metabotropic glutamate receptor 4 signature III	10.37 1.15e-22 131-147
1769	IPB000008B	C2 domain	17.91 3.02e-10 226-243
1769	IPB000008C	C2 domain	23.37 2.80e-31 400-439
1769	IPB000008C	C2 domain	23.37 3.04e-10 265-304
1769	IPB000008D	C2 domain	14.83 8.59e-14 455-473
1769	PR00360A	C2 domain signature I	15.18 3.00e-10 398-410
1769	PR00360B	C2 domain signature II	11.64 2.33e-12 427-440
1769	PR00360B	C2 domain signature II	11.64 8.88e-13 292-305
1769	PR00399A	Synaptotagmin signature I	15.05 5.50e-11 236-251
1769	PR00399B	Synaptotagmin signature II	14.30 5.50e-10 251-264
1769	PR00399B	Synaptotagmin signature II	14.30 7.92e-12 385-398
1769	PR00399C	Synaptotagmin signature III	15.89 1.63e-10 308-323
1769	PR00399D	Synaptotagmin signature IV	12.72 6.33e-10 328-338
1770	IPB000534A	Semialdehyde dehydrogenase	15.79 4.21e-09 287-304
1771	IPB001195	Glycophorin A	7.52 6.07e-10 717-745
1771	IPB001359H	Synapsin	22.58 7.99e-09 871-921
1771	IPB001514D	RNA polymerases D/30 to 40 Kd subunits	19.99 9.43e-09 1326-1352
1771	IPB002126A	Cadherin domain	14.68 4.15e-11 412-428
1771	IPB002126B	Cadherin domain	12.04 1.50e-09 232-249
1771	IPB002126B	Cadherin domain	12.04 3.25e-12 448-465
1771	IPB002126B	Cadherin domain	12.04 7.25e-09 123-140
1771	PR00205A	Cadherin signature I	17.38 5.66e-10 293-312
1771	PR00205A	Cadherin signature I	17.38 7.84e-11 75-94
1771	PR00205B	Cadherin signature II	20.09 2.73e-09 135-164
1771	PR00205B	Cadherin signature II	20.09 4.06e-10 460-489
1771	PR00205B	Cadherin signature II	20.09 8.80e-15 244-273
1771	PR00205C	Cadherin signature III	13.59 7.75e-09 317-329
1771	PR00205D	Cadherin signature IV	12.22 3.42e-14 439-458
1771	PR00205D	Cadherin signature IV	12.22 3.83e-12 223-242
1771	PR00205D	Cadherin signature IV	12.22 6.40e-12 544-563
1771	PR00205D	Cadherin signature IV	12.22 6.71e-11 331-350
1771	PR00205D	Cadherin signature IV	12.22 7.51e-10 114-133
1771	PR00205E	Cadherin signature V	10.82 4.86e-09 458-471
1771	PR00205F	Cadherin signature VI	19.57 1.95e-11 408-434
1771	PR00205F	Cadherin signature VI	19.57 2.50e-15 513-539
1771	PR00205F	Cadherin signature VI	19.57 3.65e-12 300-326
1771	PR00205G	Cadherin signature VII	13.05 2.65e-09 334-351
1771	PR00205G	Cadherin signature VII	13.05 4.65e-11 226-243
1771	PR00205G	Cadherin signature VII	13.05 7.91e-10 442-459
1771	PR00205G	Cadherin signature VII	13.05 9.57e-14 547-564

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SEQ ID NO:	Database entry ID	Description	Results*
1771	PR01157D	P2 purinoceptor signature IV	16.03 5.42e-09 815-827
1771	PR01383B	Claudin-10 signature II	5.36 5.05e-09 724-736
1774	IPB000301B	Transmembrane 4 family	18.74 4.68e-26 492-527
1774	IPB000301D	Transmembrane 4 family	26.02 7.30e-23 662-702
1774	PR00259B	Transmembrane four family signature II	13.09 3.03e-17 486-512
1774	PR00259C	Transmembrane four family signature III	16.39 5.76e-19 513-541
1774	PR00259D	Transmembrane four family signature IV	14.90 8.54e-18 676-702
1775	IPB000276A	Rhodopsin-like GPCR superfamily	11.56 1.95e-10 111-122
1775	IPB000276A	Rhodopsin-like GPCR superfamily	11.56 5.50e-09 199-210
1775	PR00237E	Rhodopsin-like GPCR superfamily signature V	13.03 3.90e-10 280-303
1775	PR00245A	Olfactory receptor signature I	10.98 1.90e-10 85-96
1775	PR00245A	Olfactory receptor signature I	10.98 2.50e-10 173-184
1775	PR00245B	Olfactory receptor signature II	13.73 1.00e-10 210-222
1775	PR00245B	Olfactory receptor signature II	13.73 8.71e-09 122-134
1775	PR00245C	Olfactory receptor signature III	14.65 4.91e-15 257-273
1775	PR00245D	Olfactory receptor signature IV	9.34 8.41e-13 317-326
1775	PR00534A	Melanocortin receptor family signature I	12.77 9.56e-11 44-56
1778	IPB000920C	Myelin P0 protein	15.78 2.33e-09 160-212
1778	IPB001388	Synaptobrevin	26.97 7.60e-30 115-169
1778	PR00219A	Synaptobrevin signature I	10.78 1.35e-11 118-137
1778	PR00219B	Synaptobrevin signature II	9.91 5.30e-09 138-157
1778	PR00219C	Synaptobrevin signature III	6.91 2.20e-13 20-39
1780	IPB000353B	Class II histocompatibility antigen, beta chain, beta-1 domain	19.16 4.96e-12 177-226
1780	IPB000353C	Class II histocompatibility antigen, beta chain, beta-1 domain	20.11 9.18e-10 228-282
1780	IPB001039A	Major histocompatibility complex protein, Class I	17.17 1.00e-40 15-68
1780	IPB001039C	Major histocompatibility complex protein, Class I	19.82 8.08e-12 151-204
1780	IPB001039D	Major histocompatibility complex protein, Class I	16.49 1.00e-40 229-283
1780	IPB003006A	Immunoglobulin and major histocompatibility complex domain	17.51 3.25e-18 198-220
1780	IPB003006B	Immunoglobulin and major histocompatibility complex domain	20.23 5.50e-28 235-272
1780	IPB003363E	Glycoprotein GG/GX	13.35 2.18e-10 282-314
1782	IPB000084A	PE N-terminus	14.90 3.44e-09 644-691
1782	IPB000258G	Bacterial ice-nucleation proteins octamer repeat	8.61 4.96e-09 681-734
1782	IPB000258H	Bacterial ice-nucleation proteins octamer repeat	10.13 6.03e-09 719-773
1782	IPB000765	GTP1/OBG family	26.91 9.84e-10 449-492
1782	IPB000790B	ATP synthase alpha subunit, C-terminal	10.45 9.64e-10 424-467
1782	IPB001140A	ABC transporter transmembrane region	21.73 2.42e-18 437-483
1782	IPB001140B	ABC transporter transmembrane region	15.62 7.70e-12 555-593
1782	IPB001482B	Bacterial type II secretion system protein E	12.05 3.70e-09 447-469
1782	PR00300A	ATP-dependent Clp protease ATP-binding subunit signature I	7.82 8.27e-09 451-469
1782	PR00449A	Transforming protein P21 ras signature I	12.48 1.67e-09 449-470
1782	PR00671B	Inhibin beta B chain signature II	4.29 9.41e-09 396-415
1783	IPB000175A	Sodium:neurotransmitter symporter family	16.29 1.00e-40 211-260
1783	IPB000175B	Sodium:neurotransmitter symporter family	19.12 3.37e-32 298-332

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SEQ ID NO:	Database entry ID	Description	Results*
1783	IPB000175C	Sodium:neurotransmitter symporter family	15.09 3.75e-13 385-436
1783	IPB000175D	Sodium:neurotransmitter symporter family	23.45 1.00e-40 451-503
1783	IPB000175E	Sodium:neurotransmitter symporter family	21.88 1.67e-30 544-583
1783	IPB000175F	Sodium:neurotransmitter symporter family	25.63 1.00e-30 639-678
1783	IPB000175G	Sodium:neurotransmitter symporter family	16.18 6.32e-20 700-722
1783	PR00176A	Sodium/chloride neurotransmitter symporter signature I	16.97 5.50e-24 211-232
1783	PR00176B	Sodium/chloride neurotransmitter symporter signature II	7.07 2.13e-22 240-259
1783	PR00176C	Sodium/chloride neurotransmitter symporter signature III	10.57 3.16e-23 283-309
1783	PR00176D	Sodium/chloride neurotransmitter symporter signature IV	8.96 7.92e-21 412-429
1783	PR00176E	Sodium/chloride neurotransmitter symporter signature V	11.14 3.84e-19 494-514
1783	PR00176F	Sodium/chloride neurotransmitter symporter signature VI	11.11 9.57e-20 548-567
1783	PR00176G	Sodium/chloride neurotransmitter symporter signature VII	13.12 7.67e-16 630-650
1783	PR00176H	Sodium/chloride neurotransmitter symporter signature VIII	15.94 4.52e-16 670-690
1783	PR01204A	Glycine neurotransmitter transporter type 1 (GLYT-1) signature I	15.11 3.25e-18 187-200
1783	PR01204B	Glycine neurotransmitter transporter type 1 (GLYT-1) signature II	12.89 1.37e-15 201-211
1783	PR01204C	Glycine neurotransmitter transporter type 1 (GLYT-1) signature III	12.34 1.60e-16 335-347
1783	PR01204D	Glycine neurotransmitter transporter type 1 (GLYT-1) signature IV	10.51 6.86e-18 349-364
1784	IPB001627K	Sema domain	13.76 3.02e-09 662-674
1784	IPB002165D	Plexin repeat	14.72 1.15e-10 662-674
1784	PR01319A	Glial cell line-derived neurotrophic factor receptor alpha 3 signature I	3.85 7.08e-09 27-39
1785	IPB000647A	CTF/NF-I family	11.22 1.00e-40 644-693
1785	IPB000647B	CTF/NF-I family	10.06 2.14e-30 694-718
1785	IPB000647C	CTF/NF-I family	9.27 1.00e-40 724-765
1785	IPB000647D	CTF/NF-I family	12.61 1.20e-32 766-790
1785	IPB000647E	CTF/NF-I family	12.21 9.18e-38 791-821
1786	IPB000483	Leucine rich repeat C-terminal domain	11.18 4.54e-10 675-689
1786	PR00019A	Leucine-rich repeat signature I	11.72 4.67e-10 243-256
1786	PR00019A	Leucine-rich repeat signature I	11.72 6.45e-09 434-447
1786	PR00019B	Leucine-rich repeat signature II	11.42 4.27e-11 431-444
1786	PR00019B	Leucine-rich repeat signature II	11.42 5.09e-09 479-492
1786	PR00019B	Leucine-rich repeat signature II	11.42 7.55e-09 597-610
1786	PR00019B	Leucine-rich repeat signature II	11.42 8.64e-09 240-253
1786	PR00364D	Disease resistance protein signature IV	14.89 4.86e-09 188-204
1789	PR00702F	Acriflavin resistance protein family signature VI	14.03 1.46e-17 49-72
1789	PR00702G	Acriflavin resistance protein family signature VII	10.67 6.00e-21 74-97
1789	PR00702H	Acriflavin resistance protein family signature VIII	14.64 3.67e-14 153-170
1789	PR00702I	Acriflavin resistance protein family signature IX	16.75 1.39e-15 216-230

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SEQ ID NO:	Database entry ID	Description	Results*
1790	PR00797F	Streptopain (C10) cysteine protease family signature VI	11.89 8.81e-09 41-62
1791	IPB000849D	GlpT family of transporters	22.39 9.25e-31 55-91
1791	IPB000849E	GlpT family of transporters	19.05 2.88e-36 108-145
1791	IPB000849F	GlpT family of transporters	15.06 8.00e-20 162-179
1792	IPB000917C	Sulfatase	13.32 4.67e-11 593-603
1792	IPB003661A	His Kinase A domain	9.35 1.60e-09 244-253
1796	IPB000203A	GPS domain	18.40 6.63e-12 903-933
1796	IPB000203B	GPS domain	13.98 9.12e-12 988-1009
1796	IPB000483	Leucine rich repeat C-terminal domain	11.18 6.04e-11 371-385
1796	IPB000832C	G-protein coupled receptors family 2 (secretin-like)	19.53 7.33e-09 988-1017
1796	PR00019A	Leucine-rich repeat signature I	11.72 1.00e-09 315-328
1796	PR00019B	Leucine-rich repeat signature II	11.42 8.00e-10 312-325
1798	IPB002208C	SecY protein	15.51 4.15e-17 30-50
1798	IPB002208D	SecY protein	22.30 2.29e-36 82-118
1798	PR00303C	Preprotein translocase SecY subunit signature III	15.05 7.84e-19 34-57
1798	PR00303D	Preprotein translocase SecY subunit signature IV	15.48 1.95e-22 72-97
1798	PR00303E	Preprotein translocase SecY subunit signature V	14.43 7.19e-23 98-121
1798	PR00825B	Vespid venom allergen phospholipase A1 signature II	13.74 9.40e-09 234-254
1800	PR00081A	Glucose/ribitol dehydrogenase family signature I	10.07 9.70e-12 179-196
1800	PR00669B	Inhibin alpha chain signature II	5.88 3.93e-09 80-96
1801	IPB000109C	PTR peptide transporters (PTR2)	8.21 3.74e-13 12-24
1801	IPB000109D	PTR peptide transporters (PTR2)	25.09 1.00e-29 464-511
1802	IPB000033B	Low-density lipoprotein (ldl) receptor, YWTD repeat	7.05 4.96e-11 494-504
1802	IPB000152	Aspartic acid and asparagine hydroxylation site	8.86 1.47e-14 489-504
1802	IPB001169K	Integrin beta, C-terminus	27.45 2.90e-10 970-1012
1802	IPB001774C	Delta serrate ligand	18.25 2.19e-09 973-1015
1802	IPB001881B	Calcium-binding EGF-like domain	12.28 6.68e-11 489-500
1802	IPB001969A	Eukaryotic and viral aspartic protease active site	16.37 7.00e-10 378-394
1802	PR00010C	Type II EGF-like signature III	6.98 7.10e-10 494-504
1802	PR00792B	Pepsin (A1) aspartic protease family signature II	12.65 3.25e-13 331-344
1802	PR00792C	Pepsin (A1) aspartic protease family signature III	8.65 9.31e-13 380-391
1803	IPB000729A	PMP-22/EMP/MP20 family	19.70 1.95e-09 1-22
1803	IPB000729A	PMP-22/EMP/MP20 family	19.70 2.20e-10 18-39
1803	IPB000729B	PMP-22/EMP/MP20 family	13.56 5.68e-10 49-59
1803	IPB000729C	PMP-22/EMP/MP20 family	37.83 3.47e-23 87-139
1803	IPB000729C	PMP-22/EMP/MP20 family	37.83 7.83e-22 80-132
1803	IPB000729D	PMP-22/EMP/MP20 family	18.96 4.94e-18 160-187
1803	PR01077B	Claudin signature II	14.12 8.80e-10 49-55
1803	PR01077C	Claudin signature III	13.60 9.43e-12 63-73
1804	IPB001717I	Anion exchanger family	7.53 2.07e-11 18-58
1804	IPB001717L	Anion exchanger family	14.31 9.28e-14 84-130
1804	IPB001717M	Anion exchanger family	19.47 6.23e-32 133-185

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SEQ ID NO:	Database entry ID	Description	Results*
1804	IPB001717N	Anion exchanger family	14.40 1.00e-30 183-208
1804	IPB001717O	Anion exchanger family	10.14 4.76e-16 209-236
1804	IPB001717Q	Anion exchanger family	17.70 5.77e-09 232-273
1804	PR00165F	Anion exchanger family signature VI	14.73 1.50e-11 42-49
1804	PR00165J	Anion exchanger family signature X	6.53 4.18e-09 127-135
1804	PR00165K	Anion exchanger family signature XI	12.74 6.40e-11 156-164
1804	PR00165M	Anion exchanger family signature XIII	9.29 7.26e-12 255-265
1804	PR01120D	Plant CLC chloride channel signature IV	10.53 6.46e-09 134-141
1804	PR01231E	HCO ₃ - transporter superfamily signature V	8.87 4.38e-15 40-52
1804	PR01231H	HCO ₃ - transporter superfamily signature VIII	12.16 9.18e-15 111-124
1805	IPB001394A	Ubiquitin carboxyl-terminal hydrolase family 2	12.64 3.16e-16 786-803
1805	IPB001394B	Ubiquitin carboxyl-terminal hydrolase family 2	17.87 3.05e-21 1215-1244
1805	IPB001394C	Ubiquitin carboxyl-terminal hydrolase family 2	8.52 3.50e-10 1290-1299
1805	IPB001394D	Ubiquitin carboxyl-terminal hydrolase family 2	9.19 4.60e-10 1308-1317
1806	PR01130C	Delayed-early response protein/equilibrative nucleoside transporter signature III	7.16 6.00e-09 187-210
1806	PR01130E	Delayed-early response protein/equilibrative nucleoside transporter signature V	14.23 6.07e-10 309-330
1806	PR01130F	Delayed-early response protein/equilibrative nucleoside transporter signature VI	5.34 3.54e-11 337-354
1807	IPB001919B	Cellulose-binding domain, bacterial type	14.22 2.97e-09 104-128
1810	IPB003662A	General substrate transporters	18.97 8.67e-14 736-768
1811	PR01228C	Eggshell protein signature III	5.69 3.90e-09 51-66
1813	IPB000260A	NADH-ubiquinone oxidoreductase chain 4, amino terminus	12.52 2.80e-09 16-49
1813	IPB000260A	NADH-ubiquinone oxidoreductase chain 4, amino terminus	12.52 4.66e-10 19-52
1813	IPB000444B	Xanthine/uracil permeases family	22.44 4.21e-09 51-94
1813	IPB000444B	Xanthine/uracil permeases family	22.44 4.32e-09 43-86
1813	IPB000684L	Eukaryotic RNA polymerase II heptapeptide repeat	3.49 7.25e-09 841-883
1813	IPB000822	Zinc finger, C2H2 type	14.67 1.00e-18 272-297
1813	IPB000822	Zinc finger, C2H2 type	14.67 2.71e-10 416-441
1813	IPB000822	Zinc finger, C2H2 type	14.67 7.19e-14 487-512
1813	IPB000822	Zinc finger, C2H2 type	14.67 8.00e-13 515-540
1813	IPB000822	Zinc finger, C2H2 type	14.67 8.11e-12 300-325
1813	IPB000822	Zinc finger, C2H2 type	14.67 9.05e-12 773-798
1813	IPB001457	NADH-ubiquinone/plastoquinone oxidoreductase chain 6	19.26 5.81e-09 5-46
1813	PR00048A	C2H2-type zinc finger signature I	9.94 6.25e-09 770-783
1813	PR00048A	C2H2-type zinc finger signature I	9.94 9.53e-11 269-282
1813	PR00048B	C2H2-type zinc finger signature II	5.52 6.79e-10 285-294
1813	PR00219C	Synaptobrevin signature III	6.91 6.34e-09 33-52
1815	IPB000001D	Kringle	11.31 2.02e-13 53-69
1815	IPB000001H	Kringle	12.24 5.29e-11 318-328
1815	IPB000126A	Serine proteases, V8 family	11.75 5.07e-11 53-68

Table 3B

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SEQ ID NO:	Database entry ID	Description	Results*
1815	IPB000177M	Apple domain	9.18 8.55e-16 226-260
1815	IPB000177N	Apple domain	10.17 5.21e-15 308-342
1815	IPB001254A	Serine proteases, trypsin family	9.98 1.00e-15 53-69
1815	IPB001254B	Serine proteases, trypsin family	15.01 6.29e-18 316-339
1815	PR00722A	Chymotrypsin serine protease family (S1) signature I	12.06 9.28e-15 54-69
1815	PR00722C	Chymotrypsin serine protease family (S1) signature III	10.74 8.88e-13 315-327
1815	PR00839B	V8 serine protease family signature II	11.20 6.42e-09 53-70
1817	IPB003819A	Taurine catabolism dioxygenase TauD/TfdA	10.95 3.03e-09 200-207
1817	IPB003819B	Taurine catabolism dioxygenase TauD/TfdA	21.71 5.64e-26 222-255
1817	IPB003819C	Taurine catabolism dioxygenase TauD/TfdA	11.87 2.74e-17 288-304
1817	IPB003819D	Taurine catabolism dioxygenase TauD/TfdA	27.59 4.68e-38 319-359
1819	IPB000387	Tyrosine specific protein phosphatase and dual specificity protein phosphatase family	10.77 2.38e-13 1434-1444
1819	PR00014C	Fibronectin type III repeat signature III	14.47 4.00e-09 599-617
1819	PR00014C	Fibronectin type III repeat signature III	14.47 4.86e-09 688-706
1819	PR00014C	Fibronectin type III repeat signature III	14.47 5.00e-10 1056-1074
1819	PR00014C	Fibronectin type III repeat signature III	14.47 7.00e-09 866-884
1819	PR00213E	Myelin P0 protein signature V	5.51 1.66e-09 1186-1210
1819	PR00700A	Protein tyrosine phosphatase signature I	6.05 5.80e-10 1306-1313
1819	PR00700C	Protein tyrosine phosphatase signature III	13.89 7.88e-17 1390-1407
1819	PR00700D	Protein tyrosine phosphatase signature IV	12.83 3.86e-20 1431-1449
1819	PR00700F	Protein tyrosine phosphatase signature VI	10.33 4.71e-12 1478-1488
1819	PR01371E	Salmonella/Yersinia modular tyrosine phosphatase signature V	11.71 5.98e-12 1432-1443
1820	IPB003842A	Vacuolating cytotoxin	7.27 9.28e-09 100-146
1821	IPB000276D	Rhodopsin-like GPCR superfamily	9.40 9.65e-09 405-421
1821	PR00245D	Olfactory receptor signature IV	9.34 1.53e-13 359-368
1821	PR00245E	Olfactory receptor signature V	8.96 6.88e-13 406-417
1822	IPB003861B	E4 protein	9.06 1.00e-08 34-48
1822	PR00494E	Fanconi anaemia group C protein signature V	10.42 8.26e-09 621-640
1822	PR01039A	Tryptophanyl-tRNA synthetase signature I	14.70 9.59e-09 200-216

* Results include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
912	MIF	Macrophage migration inhibitory factor (MIF)	2.4e-54	194.0	1	124-227
912	GST_C	Glutathione S-transferase, C-terminal domain	6.2e-25	92.6	2	1-45:410-525
912	GST_N	Glutathione S-transferase, N-terminal domain	1.4e-16	62.5	1	324-400
913	tsp_1	Thrombospondin type 1 domain	2.9e-23	90.7	2	124-174:181-231
913	EGF	EGF-like domain	1.6e-20	81.6	7	474-508:514-553:559-591:597-633:692-720:802-836:842-882
914	MIF	Macrophage migration inhibitory factor (MIF)	4.5e-50	179.8	1	2-101
915	MIF	Macrophage migration inhibitory factor (MIF)	6.1e-68	239.1	1	2-129
916	trypsin	Trypsin	3.8e-99	314.8	1	445-675
916	kringle	Kringle domain	4.2e-45	163.3	1	286-367
916	fn2	Fibronectin type II domain	4.5e-35	94.9	1	108-148
916	EGF	EGF-like domain	6.2e-15	63.0	2	164-197:245-278
916	fn1	Fibronectin type I domain	5.2e-11	45.0	1	202-237
917	laminin_EGF	Laminin EGF-like (Domains III and V)	2.3e-158	539.5	12	282-346:349-409:412-469:472-520:523-565:786-831:834-877:880-925:928-984:987-1036:1039-1094:1095-1139
917	laminin_Nterm	Laminin N-terminal (Domain VI)	5.9e-105	362.1	1	45-280
918	EGF	EGF-like domain	3.2e-53	190.2	9	33-68:74-110:116-151:161-197:208-243:247-282:288-323:329-362:368-404
918	CUB	CUB domain	1.1e-16	68.8	1	708-817
919	Parathyroid	Parathyroid hormone family	3.1e-82	286.6	1	46-175
920	EGF	EGF-like domain	2.2e-22	87.8	9	2-36:47-82:88-122:128-163:232-263:276-306:319-349:353-394:407-439
921	IL8	Small cytokines (intecrine/chemokine), inter	2.7e-09	35.4	1	25-65
922	Zn_carbOpept	Zinc carboxypeptidase	3.1e-119	409.5	1	149-429
922	Propep_M14	Carboxypeptidase activation peptide	5.6e-20	79.8	1	7-84
923	fibrinogen_C	Fibrinogen beta and gamma chains, C-term	1.8e-67	237.6	1	62-248
927	FKBP	FKBP-type peptidyl-prolyl cis-trans isomeras	1.3e-44	149.6	2	40-111:112-122
930	FAD_binding_4	FAD binding domain	6.5e-89	308.8	2	11-176:186-381
930	FAD-oxidase_C	FAD linked oxidases, C-terminal domain	2.6e-63	223.8	1	383-647
933	Fringe	Fringe-like	1.4e-06	-12.8	1	262-487

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
937	14-3-3	14-3-3 protein	1.1e-124	427.6	1	58-282
938	S_100	S-100/ICaBP type calcium binding domain	3.6e-23	90.4	1	65-108
938	efhand	EF hand	0.0012	25.5	1	114-142
940	ig	Immunoglobulin domain	1.2e-33	113.5	5	38-105:139-206:241-293:326-377:412-487
941	LRR	Leucine Rich Repeat	3.6e-30	113.7	8	42-63:64-87:88-112:113-136:137-160:161-184:185-208:209-232
941	LRRCT	Leucine rich repeat C-terminal domain	1.2e-07	38.9	1	242-292
943	AMP-binding	AMP-binding enzyme	1.2e-16	62.6	1	82-159
944	serpin	Serpin (serine protease inhibitor)	7e-134	455.1	1	173-532
947	RUN	RUN domain	8e-44	159.0	1	31-163
947	FYVE	FYVE zinc finger	1.6e-18	70.7	1	529-576
950	lectin_c	Lectin C-type domain	2.4e-08	41.1	1	130-234
952	Glyco_transf_8	Glycosyl transferase family 8	0.01	-47.7	1	1255-1526
953	TPR	TPR Domain	0.0044	23.7	1	171-204
956	Branch	Core-2/I-Branching enzyme	5.5e-102	352.2	1	74-306
957	fn3	Fibronectin type III domain	1.1e-15	65.6	1	30-108
958	Peptidase_M10	Matrixin	5.9e-121	415.2	1	58-225
958	hemopexin	Hemopexin	2e-58	207.5	4	305-347:349-393:398-445:447-487
962	chromo	'chromo' (CHRromatin Organization Modifier)	5.5e-09	35.7	1	64-84
964	ig	Immunoglobulin domain	1.8e-05	22.6	1	34-115
967	7tm_1	7 transmembrane receptor (rhodopsin family)	2.1e-26	86.0	2	41-154:161-237
968	adh_zinc	Zinc-binding dehydrogenases	7.4e-60	212.3	1	179-495
970	E1_dehydrog	Dehydrogenase E1 component	2.1e-183	622.7	1	129-425
971	ig	Immunoglobulin domain	9.3e-11	39.7	1	45-122
973	zf-MIZ	MIZ zinc finger	3.2e-32	120.5	1	279-331
973	SAP	SAP domain	7.4e-06	32.9	1	2-36
975	WD40	WD domain, G-beta repeat	5e-08	40.1	3	234-270:447-483:491-528
977	An_peroxidase	Animal haem peroxidase	5.6e-140	478.4	1	137-701
978	Defensin_propep	Defensin propeptide	1.9e-17	71.4	1	32-82
978	defensins	Mammalian defensin	8.6e-05	23.3	1	95-123
981	ig	Immunoglobulin domain	3.6e-06	24.9	1	49-130
982	ig	Immunoglobulin domain	1.2e-09	36.1	1	36-112
985	tsp_1	Thrombospondin type 1 domain	0.0075	17.1	1	151-206
987	LRR	Leucine Rich Repeat	1.1e-58	208.4	12	78-101:102-125:126-149:150-173:174-197:198-221:222-245:246-269:270-293:294-317:318-341:342-

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
						365
988	fer4_NifH	4Fe-4S iron sulfur cluster binding proteins	0.0015	15.9	1	110-134
988	ParA	ParA family ATPase	0.006	-0.3	1	177-283
989	vwd	von Willebrand factor type D domain	1.6e-37	134.9	1	364-514
989	vwc	von Willebrand factor type C domain	5.3e-35	129.7	5	50-105:108-163:166-224:238-289:301-357
989	TIL	Trypsin Inhibitor like cysteine rich domain	8.9e-06	32.6	1	629-682
992	ig	Immunoglobulin domain	9.6e-17	59.0	2	34-111:150-220
994	ig	Immunoglobulin domain	1.6e-28	97.0	3	43-110:143-197:230-291
995	SCP	SCP-like extracellular protein	4.7e-41	149.8	1	4-173
996	ig	Immunoglobulin domain	8.9e-06	23.7	2	73-123:153-206
999	RNase_PH	3' exoribonuclease family	1.5e-28	108.3	1	264-469
1000	ig	Immunoglobulin domain	2.6e-05	22.2	1	38-102
1002	zf-C2H2	Zinc finger, C2H2 type	7.6e-54	192.3	7	183-205:211-233:239-261:267-289:295-317:323-345:351-373
1003	zf-C2H2	Zinc finger, C2H2 type	2.1e-114	393.5	16	260-282:297-319:325-347:353-375:381-403:409-431:437-459:465-487:493-515:521-543:549-571:577-599:605-627:633-655:661-683:689-711
1007	LIM	LIM domain	1.5e-37	138.2	3	390-448:450-507:510-576
1010	zf-C2H2	Zinc finger, C2H2 type	4.2e-06	33.7	3	2-24:29-52:154-177
1011	60s_ribosomal	60s Acidic ribosomal protein	1.1e-28	94.4	2	1-22:25-89
1012	abhydrolase_2	Phospholipase/Carboxylesterase	1.3e-24	95.2	1	9-213
1016	Anti_proliferat	BTG1 family	3.6e-73	256.5	1	11-253
1017	zf-C2H2	Zinc finger, C2H2 type	9.3e-71	248.5	11	147-169:213-231:269-291:325-347:353-375:381-403:409-431:437-459:465-487:493-515:521-543
1017	KRAB	KRAB box	1.7e-21	84.8	1	42-122
1020	LIM	LIM domain	7e-36	132.6	4	78-136:139-197:200-256:259-318
1024	zf-C2H2	Zinc finger, C2H2 type	3.3e-53	190.2	10	156-183:184-206:212-234:240-262:268-290:296-318:324-346:352-374:380-402:408-

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
						430
1024	KRAB	KRAB box	2.1e-42	154.3	1	15-77
1025	RAG2	Recombination activating protein 2	0	1380.2	1	1-527
1026	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.7e-09	33.9	1	16-54
1029	Keratin_B2	Keratin, high sulfur B2 protein	3.8e-06	16.4	2	5-149:150-281
1031	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	1.5e-106	367.4	1	5-165
1035	zf-C2H2	Zinc finger, C2H2 type	9.9e-114	391.2	17	100-122:132-154:160-182:188-210:216-238:244-266:272-294:300-322:328-350:356-378:384-406:412-434:440-462:468-490:496-518:524-546:552-574
1035	KRAB	KRAB box	2.3e-16	67.8	1	4-54
1038	Sulfate_transp	Sulfate transporter family	4.3e-103	355.9	2	2-284:441-751
1038	STAS	STAS domain	4.8e-20	80.0	1	774-987
1039	ubiquitin	Ubiquitin family	1.4e-09	39.6	1	55-126
1042	ig	Immunoglobulin domain	1.2e-30	103.8	5	62-129:163-229:264-316:349-400:433-501
1043	UPAR_LY6	u-PAR/Ly-6 domain	9.1e-59	208.7	1	63-190
1047	MHC_I	Class I Histocompatibility antigen, domains	3.2e-147	502.5	1	25-203
1047	ig	Immunoglobulin domain	0.057	11.4	1	220-285
1050	ig	Immunoglobulin domain	2.3e-09	35.2	1	38-110
1051	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	0.0019	-4.7	1	4-194
1054	SRCR	Scavenger receptor cysteine-rich domain	6.2e-25	96.3	1	722-820
1055	P2X_receptor	ATP P2X receptor	9.3e-302	1015.9	1	13-388
1057	zona_pellucida	Zona pellucida-like domain	1.1e-80	281.5	1	268-538
1057	trefoil	Trefoil (P-type) domain	0.02	9.1	1	224-262
1058	Aa_trans	Transmembrane amino acid transporter protein	9.4e-09	42.5	1	30-389
1059	7tm_1	7 transmembrane receptor (rhodopsin family)	2.1e-13	44.8	1	33-280
1060	Na_sulph_symp	Sodium:sulfate symporter transmembrane	1.2e-143	490.7	1	16-554
1064	ERG4_ERG24	Ergosterol biosynthesis ERG4/ERG24 family	1.1e-103	357.8	1	7-350
1066	ig	Immunoglobulin domain	4.7e-16	56.8	3	42-95:135-192:231-288
1067	7tm_1	7 transmembrane receptor (rhodopsin family)	2.3e-33	108.1	1	28-266
1069	pkinase	Protein kinase domain	4.9e-68	239.4	1	298-578
1069	Activin_recip	Activin types I and II receptor domain	1.6e-27	104.8	1	20-107

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1070	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	0.00018	13.2	1	3-177
1071	MHC_I	Class I Histocompatibility antigen, domains	4.4e-14	55.1	1	24-196
1071	ig	Immunoglobulin domain	2.8e-07	28.5	1	218-284
1073	sugar_tr	Sugar (and other) transporter	0.028	-126.7	1	48-528
1074	sugar_tr	Sugar (and other) transporter	0.028	-126.7	1	136-616
1075	ank	Ank repeat	1.7e-45	164.6	6	31-63:64-96:97-129:130-162:163-195:196-228
1076	7tm_1	7 transmembrane receptor (rhodopsin family)	5.6e-12	40.2	1	178-349
1077	sugar_tr	Sugar (and other) transporter	0.0032	-100.1	1	46-470
1079	G_glu_transpept	Gamma-glutamyltranspeptidase	2.8e-05	-144.9	1	122-500
1080	TPR	TPR Domain	2.3e-19	77.8	5	28-61:68-101:108-141:148-181:188-221
1081	ACAT	Sterol O-acyltransferase	1.9e-32	121.3	1	300-406
1082	WD40	WD domain, G-beta repeat	2.3e-16	67.8	7	1015-1050:1059-1097:1115-1151:1158-1194:1203-1240:1246-1281:1293-1329
1083	pkinase	Protein kinase domain	4.9e-57	202.9	2	248-492:537-564
1083	Activin_rec	Activin types I and II receptor domain	3.1e-36	133.8	1	26-127
1084	pkinase	Protein kinase domain	4.9e-57	202.9	2	310-554:599-626
1084	Activin_rec	Activin types I and II receptor domain	3.1e-36	133.8	1	26-127
1086	C2	C2 domain	1.7e-06	35.0	1	233-316
1087	Cache	Cache domain	1.5e-25	96.2	2	557-650:960-985
1088	Glyco_hydro_31	Glycosyl hydrolases family 31	4.9e-268	903.8	2	1-92:114-636
1090	HMG_box	HMG (high mobility group) box	3.8e-32	120.2	1	681-749
1091	serpin	Serpin (serine protease inhibitor)	3.1e-195	662.0	1	315-683
1092	trypsin	Trypsin	0.0044	12.4	1	406-526
1094	Aa_trans	Transmembrane amino acid transporter protein	0.0042	-25.4	1	141-551
1097	ATP-synt_C	ATP synthase subunit C	3.3e-18	73.9	1	72-140
1098	aconitase	Aconitase family (aconitate hydratase)	1.4e-198	651.7	2	162-241:321-744
1098	Aconitase_C	Aconitase C-terminal domain	8.9e-72	251.9	1	872-1043
1103	PAP2	PAP2 superfamily	6.3e-15	63.0	1	89-236
1104	ig	Immunoglobulin domain	1.4e-20	71.3	2	80-148:183-251
1106	TCTP	Translationally controlled tumor protein	3.5e-93	323.0	1	1-166

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1109	efhand	EF hand	1.2e-13	58.8	3	33-61:102-130:138-166
1110	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	1.8e-13	58.2	1	92-146
1112	ldl_recept_a	Low-density lipoprotein receptor domain	0.00073	26.3	1	115-153
1112	CUB	CUB domain	0.002	-3.5	1	9-109
1115	7tm_1	7 transmembrane receptor (rhodopsin family)	3.9e-21	69.3	1	139-317
1116	7tm_1	7 transmembrane receptor (rhodopsin family)	1.4e-24	80.3	3	2-28:114-275:348-363
1119	tsp_1	Thrombospondin type 1 domain	4.5e-38	139.9	10	149-198:306-364:571-626:631-696:707-761:841-889:970-1021:1099-1148:1219-1269:1342-1398
1120	HMG14_17	HMG14 and HMG17	1.3e-34	128.4	1	2-86
1125	ig	Immunoglobulin domain	4.7e-20	69.7	3	84-153:185-255:292-347
1127	ig	Immunoglobulin domain	1.6e-10	38.9	1	42-112
1131	C2	C2 domain	5.7e-19	76.5	2	167-257:667-750
1133	7tm_1	7 transmembrane receptor (rhodopsin family)	6.9e-29	93.9	1	104-352
1134	MIP	Major intrinsic protein	3.9e-40	125.5	3	80-189:197-262:308-325
1136	sugar_tr	Sugar (and other) transporter	0.024	-124.9	1	23-504
1137	ATP-synt_C	ATP synthase subunit C	3.3e-35	130.4	2	14-79:90-155
1138	DHDPS	Dihydrodipicolinate synthetase family	4.4e-32	120.0	1	34-325
1139	SSF	Sodium:solute symporter family	1.5e-48	174.7	2	50-461:569-953
1143	7tm_1	7 transmembrane receptor (rhodopsin family)	2.2e-50	162.2	1	78-332
1145	PID	Phosphotyrosine interaction domain (PTB/PID)	1.9e-94	327.2	2	488-627:661-782
1145	WW	WW domain	2.5e-08	41.1	1	373-401
1148	C2	C2 domain	2.1e-30	114.4	2	87-165:240-320
1152	7tm_1	7 transmembrane receptor (rhodopsin family)	9.6e-31	99.8	1	161-410
1153	WD40	WD domain, G-beta repeat	0.013	22.1	4	26-62:71-109:236-271:430-467
1155	aa_permeases	Amino acid permease	5.6e-06	-179.9	1	193-613
1158	dUTPase	dUTPase	5.1e-29	109.8	1	46-167
1158	MIP	Major intrinsic protein	3.8e-28	88.8	1	2-56
1158	rvp	Retroviral aspartyl protease	2.1e-22	85.1	1	179-280
1158	G-patch	G-patch domain	0.00095	25.9	1	285-329
1160	laminin_EGF	Laminin EGF-like (Domains III and V)	9.5e-132	451.1	14	299-353:356-423:426-466:490-532:535-578:584-627:630-680:683-727:1265-

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
						1308:1311-1352:1355-1401:1404-1452:1686-1730:1733-1786
1160	laminin_Nterm	Laminin N-terminal (Domain VI)	4e-77	269.6	1	47-297
1160	laminin_G	Laminin G domain	6.1e-31	116.2	3	2625-2748:3015-3138:3185-3313
1160	laminin_B	Laminin B (Domain IV)	1.1e-09	45.6	1	1517-1651
1161	EGF	EGF-like domain	2.2e-26	101.1	5	29-57:60-88:104-140:147-178:185-216
1162	interferon	Interferon alpha/beta domain	1.5e-17	71.7	1	16-171
1163	IL1	Interleukin-1 / 18	8.7e-21	82.5	1	19-159
1164	PDGF	Platelet-derived growth factor (PDGF)	1.8e-51	184.4	1	52-130
1165	IL1	Interleukin-1 / 18	3.7e-23	90.4	1	11-144
1167	Palm_thioest	Palmitoyl protein thioesterase	2.4e-216	732.1	1	28-282
1168	serpin	Serpin (serine protease inhibitor)	1.6e-202	686.2	1	47-415
1170	Defensin_propep	Defensin propeptide	1.2e-26	102.0	1	38-90
1170	defensins	Mammalian defensin	7.3e-14	59.5	1	103-131
1172	Y_phosphatase	Protein-tyrosine phosphatase	1.8e-110	380.4	1	271-499
1179	Metallophos	Calcineurin-like phosphoesterase	1.1e-11	52.3	1	70-285
1184	MHC_I	Class I Histocompatibility antigen, domains	6.2e-06	-5.9	1	29-205
1187	PLA2_B	Lysophospholipase catalytic domain	8.3e-53	188.9	1	357-800
1187	C2	C2 domain	1.6e-06	35.1	1	46-129
1189	lipocalin	Lipocalin / cytosolic fatty-acid binding	2.6e-39	144.0	1	39-188
1189	Kunitz_BPTI	Kunitz/Bovine pancreatic trypsin inhibito	4.7e-23	90.0	2	231-273:274-319
1190	ig	Immunoglobulin domain	4e-07	37.1	1	38-116
1191	ig	Immunoglobulin domain	4e-07	37.1	1	38-116
1200	zf-DHHC	DHHC zinc finger domain	3.7e-15	63.8	1	87-149
1201	KRAB	KRAB box	6.6e-22	86.2	1	33-73
1202	KRAB	KRAB box	6.6e-22	86.2	1	33-73
1204	trypsin	Trypsin	3e-31	117.2	1	56-239
1212	LRR	Leucine Rich Repeat	2.5e-54	193.9	15	73-96:97-122:123-149:150-175:176-195:197-220:221-246:247-270:292-317:318-337:339-362:363-388:389-408:410-433:434-459
1213	Zn_carbOpept	Zinc carboxypeptidase	4.3e-62	219.7	1	50-288
1221	C1q	C1q domain	3.4e-41	150.3	1	134-258
1221	Collagen	Collagen triple helix repeat	2.6e-10	47.7	1	41-100

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
		(20 copies)				
1223	pkinase	Protein kinase domain	9e-75	261.8	1	158-417
1223	SH3	SH3 domain	0.019	7.4	1	423-478
1223	UBA	UBA/TS-N domain	0.037	20.6	1	987-1026
1224	vwa	von Willebrand factor type A domain	1.2e-05	29.0	1	51-242
1225	abhydrolase	alpha/beta hydrolase fold	3.7e-12	53.8	1	111-390
1227	lectin_c	Lectin C-type domain	9.6e-29	108.9	1	54-166
1237	fibrinogen_C	Fibrinogen beta and gamma chains, C-term	1.5e-09	-1.3	1	242-385
1257	LRR	Leucine Rich Repeat	9e-65	228.6	14	78-101:102-125:126-149:150-173:174-197:198-221:222-245:246-269:270-293:294-317:318-341:342-365:366-389:390-413
1257	LRRCT	Leucine rich repeat C-terminal domain	0.011	22.3	1	423-475
1263	Pep_M12B_prop ep	Reprolysin family propeptide	1.8e-28	108.1	1	75-191
1263	disintegrin	Disintegrin	2.7e-11	51.0	1	419-494
1263	Reprolysin	Reprolysin (M12B) family zinc metallo	7.3e-07	-22.2	1	206-402
1266	Clusterin	Clusterin	2.3e-298	1004.6	1	2-394
1267	serpin	Serpin (serine protease inhibitor)	3.8e-140	479.0	1	80-425
1268	serpin	Serpin (serine protease inhibitor)	6.8e-162	551.2	1	98-461
1269	COX6C	Cytochrome c oxidase subunit VIc	2.3e-38	140.9	1	1-75
1273	Rhodanese	Rhodanese-like domain	1.5e-48	174.7	2	16-138:165-266
1274	trypsin	Trypsin	2.9e-80	280.1	1	121-346
1279	Calpain_III	Calpain large subunit, domain III	1.5e-25	98.3	1	30-179
1287	zf-C2H2	Zinc finger, C2H2 type	4.4e-66	233.0	9	173-195:201-223:229-251:257-279:285-307:313-335:341-363:369-391:397-419
1287	KRAB	KRAB box	4.9e-23	90.0	1	14-54
1294	vwc	von Willebrand factor type C domain	1.3e-09	45.4	1	69-127
1295	zf-C2H2	Zinc finger, C2H2 type	5e-50	179.6	8	263-285:319-341:347-369:375-397:403-425:431-453:459-481:487-510
1295	KRAB	KRAB box	8.9e-26	99.1	1	8-48
1296	zf-C2H2	Zinc finger, C2H2 type	3.2e-113	389.6	13	190-212:218-240:246-268:274-296:302-324:330-352:358-380:386-408:414-436:442-

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
						464:470-492:498-520:526-548
1296	KRAB	KRAB box	6.7e-28	106.1	1	14-54
1299	hemopexin	Hemopexin	7e-25	96.1	4	279-322:324-367:369-415:417-461
1299	Peptidase_M10	Matrixin	8.4e-14	58.8	1	1-176
1305	DUF25	Domain of unknown function DUF25	5.3e-76	265.9	1	40-162
1307	kazal	Kazal-type serine protease inhibitor domain	1.3e-12	55.3	1	21-68
1309	Defensin_propep	Defensin propeptide	1.2e-26	102.0	1	74-126
1309	defensins	Mammalian defensin	7.3e-14	59.5	1	139-167
1312	ras	Ras family	2.7e-59	210.4	1	64-253
1314	zf-C2H2	Zinc finger, C2H2 type	1.1e-51	185.1	8	163-185:191-213:219-241:247-269:275-297:303-325:331-353:359-381
1315	Keratin_B2	Keratin, high sulfur B2 protein	0.0035	-30.0	1	13-154
1316	Keratin_B2	Keratin, high sulfur B2 protein	3.6e-15	63.8	1	23-154
1317	Keratin_B2	Keratin, high sulfur B2 protein	8.2e-20	79.2	2	20-163:164-295
1319	zf-C2H2	Zinc finger, C2H2 type	2.9e-52	187.1	7	33-55:61-83:89-111:117-139:145-167:173-195:201-223
1321	Keratin_B2	Keratin, high sulfur B2 protein	0.00014	-8.3	1	23-193
1331	ig	Immunoglobulin domain	9.7e-06	32.5	1	24-78
1332	Kunitz_BPTI	Kunitz/Bovine pancreatic trypsin inhibitor	2.2e-18	74.5	1	76-126
1333	zf-C2H2	Zinc finger, C2H2 type	4.6e-55	196.3	7	199-221:227-249:255-277:283-305:311-333:339-361:367-389
1333	KRAB	KRAB box	5.8e-24	93.0	1	6-46
1336	vwa	von Willebrand factor type A domain	0.0038	-8.1	1	32-193
1337	vwa	von Willebrand factor type A domain	0.0038	-8.1	1	32-193
1339	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	0.0088	-16.3	1	4-203
1340	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	0.0019	-4.7	1	4-194
1343	ig	Immunoglobulin domain	1.5e-13	58.5	2	81-158:204-278
1347	ig	Immunoglobulin domain	1.2e-07	38.9	2	168-226:276-330
1348	ig	Immunoglobulin domain	1.5e-18	75.1	3	157-217:269-325:373-427
1353	LRR	Leucine Rich Repeat	2e-39	144.4	9	120-143:144-167:168-191:192-

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
						215:216-239:240-263:264-287:311-334:335-358
1353	LRRNT	Leucine rich repeat N-terminal domain	0.0066	23.1	1	92-119
1356	ig	Immunoglobulin domain	2.1e-17	71.3	3	37-106:138-208:245-300
1357	CD36	CD36 family	3.9e-231	781.3	1	5-445
1358	DUF139	Cysteine rich repeat (DUF139)	1.2e-08	42.2	4	195-211:245-261:288-304:316-332
1359	ig	Immunoglobulin domain	1.6e-06	35.1	2	41-124:156-230
1359	Gag_MA	Matrix protein (MA), p15	0.0044	-25.2	1	291-429
1360	ion_trans	Ion transport protein	0.0031	24.2	1	285-445
1363	spectrin	Spectrin repeat	9.5e-22	85.7	6	17-121:124-226:229-340:372-476:678-785:788-896
1366	C1q	C1q domain	2.1e-31	117.8	1	266-390
1366	Collagen	Collagen triple helix repeat (20 copies)	0.00029	19.8	1	182-241
1367	maseA	Pancreatic ribonuclease	1.1e-34	128.7	1	27-132
1368	3HCDH_N	3-hydroxyacyl-CoA dehydrogenase, NAD binding	0.0021	-60.2	1	50-141
1371	voltage_CLC	Voltage gated chloride channel	3.1e-199	675.3	1	92-528
1371	CBS	CBS domain	1.2e-24	95.4	2	559-617:761-814
1375	Peptidase_C1	Papain family cysteine protease	1e-120	414.5	1	114-332
1376	7tm_1	7 transmembrane receptor (rhodopsin family)	2.6e-50	180.6	1	48-454
1378	7tm_2	7 transmembrane receptor (Secretin family)	4.9e-09	32.5	1	250-500
1380	MAGE	MAGE family	1.4e-91	317.7	1	3-231
1381	ion_trans	Ion transport protein	0.066	16.8	1	158-323
1382	ig	Immunoglobulin domain	7e-12	52.9	2	37-128:160-241
1385	MHC_I	Class I Histocompatibility antigen, domains	9.3e-06	-8.4	1	29-204
1388	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	7e-88	305.4	1	45-184
1390	7tm_1	7 transmembrane receptor (rhodopsin family)	5.3e-06	21.2	1	1-210
1393	7tm_1	7 transmembrane receptor (rhodopsin family)	1.6e-12	55.0	1	99-329
1397	fn3	Fibronectin type III domain	4.7e-78	272.7	5	533-619:631-717:734-833:854-939:951-1039
1397	ig	Immunoglobulin domain	3.7e-42	153.5	5	154-227:261-318:362-418:453-511:1253-1316
1404	ig	Immunoglobulin domain	2.9e-08	40.9	2	42-99:139-198
1409	ig	Immunoglobulin domain	8.1e-30	112.5	3	142-199:263-321:359-438
1414	mito_carr	Mitochondrial carrier	3.5e-64	226.7	3	40-130:137-

Table 4A
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SEQ ID	Model	Description	E-value	Score	Repeats	Position
		protein				227:238-322
1416	ig	Immunoglobulin domain	0.0011	25.6	1	57-112
1417	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	6.6e-06	33.1	1	27-67
1418	Synaptophysin	Synaptophysin / synaptoporin	9.3e-73	255.1	1	27-273
1419	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	5.2e-18	73.3	1	4-165
1421	Ammonium_transp	Ammonium Transporter Family	8.5e-18	72.6	1	25-383
1423	rnaseA	Pancreatic ribonuclease	4.1e-29	110.1	1	32-136
1427	LRR	Leucine Rich Repeat	4.5e-26	100.0	6	3-26:27-50:51-74:76-99:100-123:124-144
1427	fn3	Fibronectin type III domain	2.7e-08	41.0	1	334-417
1427	ig	Immunoglobulin domain	2.4e-07	37.9	1	225-283
1427	LRRCT	Leucine rich repeat C-terminal domain	7.2e-06	32.9	1	164-209
1428	GRAM	GRAM domain	0.067	13.1	1	177-245
1435	Rhomboid	Rhomboid family	1.5e-45	164.8	1	169-326
1437	Sema	Sema domain	7e-202	684.1	1	102-513
1437	tsp_1	Thrombospondin type 1 domain	1.1e-42	155.3	6	589-637:644-695:702-746:833-883:890-940:945-985
1437	PSI	Plexin repeat	2.5e-14	61.0	1	531-578
1438	ank	Ankyrin repeat	2e-15	64.7	3	336-368:383-418:468-498
1438	ion_trans	Ion transport protein	9.4e-07	35.9	1	615-817
1439	ank	Ankyrin repeat	3.3e-12	54.0	3	417-449:464-499:549-579
1439	ion_trans	Ion transport protein	9.4e-07	35.9	1	696-898
1442	LRR	Leucine Rich Repeat	3.2e-20	80.6	5	57-80:81-104:105-128:129-152:153-176
1442	LRRCT	Leucine rich repeat C-terminal domain	2.3e-07	37.9	1	186-240
1442	LRRNT	Leucine rich repeat N-terminal domain	0.00013	28.8	1	27-55
1443	7tm_2	7 transmembrane receptor (Secretin family)	7.2e-23	89.4	1	166-476
1443	HMG_box	HMG (high mobility group) box	3.1e-05	30.8	1	3-76
1443	GPS	Latrophilin/CL-1-like GPS domain	0.0066	19.1	1	110-162
1444	DUF214	Predicted permease	0.0045	-15.6	1	136-276
1452	mito_carr	Mitochondrial carrier protein	8.4e-58	205.5	2	27-123:124-217
1454	mito_carr	Mitochondrial carrier protein	0.00049	22.3	2	79-179:198-287
1455	WD40	WD domain, G-beta repeat	2.7e-26	100.8	4	64-99:105-141:235-273:279-315
1456	Furin-like	Furin-like cysteine rich	6.1e-89	308.9	1	172-328

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
		region				
1456	Recep_L_domain	Receptor L domain	3.1e-80	280.0	2	46-169:345-471
1456	pkinase	Protein kinase domain	7e-65	229.0	1	986-1258
1462	Peptidase_M10	Matrixin	1.5e-79	277.7	1	62-227
1462	hemopexin	Hemopexin	1.4e-10	48.6	1	309-350
1463	Armadillo_seg	Armadillo/beta-catenin-like repeat	0.028	21.0	4	549-591:641-685:686-737:738-783
1466	C2	C2 domain	6.5e-07	36.4	1	219-304
1468	RTC	RNA 3'-terminal phosphate cyclase	0.0006	-	1	3-221
1476	CN_hydrolase	Carbon-nitrogen hydrolase	0.0014	-83.3	1	64-341
1477	zf-C2H2	Zinc finger, C2H2 type	4.2e-06	33.7	3	267-289:294-317:419-442
1478	Euk_porin	Eukaryotic porin	3.3e-06	-42.1	1	1-142
1484	BTB	BTB/POZ domain	1.8e-09	44.9	1	52-194
1487	rvt	Reverse transcriptase	5.6e-56	199.4	1	241-507
1489	Galactosyl_T_2	Galactosyltransferase	3.6e-175	595.3	1	97-404
1491	GBP_C	Guanylate-binding protein, C-terminal domain	1.8e-32	117.0	1	23-125
1493	NUDIX	MutT-like domain	0.0018	23.5	1	297-439
1496	Big_2	Bacterial Ig-like domain (group 2)	4.5e-16	66.8	1	1177-1258
1497	ig	Immunoglobulin domain	9.9e-13	46.1	1	38-112
1498	aldo_ket_red	Aldo/keto reductase family	6.8e-37	126.5	2	207-237:245-359
1502	Caveolin	Caveolin	1.6e-06	13.3	1	90-262
1504	sushi	Sushi domain (SCR repeat)	8.2e-16	66.0	2	223-281:286-344
1511	zf-C2H2	Zinc finger, C2H2 type	1.1e-16	68.9	2	341-363:369-391
1511	KRAB	KRAB box	6e-05	22.1	1	231-275
1516	CBS	CBS domain	2.8e-33	124.0	3	189-243:264-317:336-389
1517	zf-C2H2	Zinc finger, C2H2 type	2.1e-128	440.0	18	279-301:307-329:335-357:363-385:391-413:419-441:447-469:475-497:503-525:868-890:896-918:924-946:952-974:980-1002:1008-1030:1036-1058:1064-1086:1092-1114
1517	KRAB	KRAB box	5.3e-69	242.7	2	74-136:684-735
1518	ig	Immunoglobulin domain	1.1e-07	29.8	1	38-102
1521	CoA_trans	Coenzyme A transferase	1.1e-161	550.5	2	42-261:271-472
1521	TGF-beta	Transforming growth factor beta like domain	6.8e-64	225.7	1	637-741
1523	Reprolysin	Reprolysin (M12B) family zinc metallo	4.4e-95	329.3	1	223-422
1523	Pep_M12B_propep	Reprolysin family propeptide	6.7e-30	112.8	1	121-234
1523	disintegrin	Disintegrin	1.1e-18	59.5	1	437-513
1523	EGF	EGF-like domain	0.0092	22.6	1	661-693
1524	DSPc	Dual specificity phosphatase, catalytic doma	3.6e-71	249.9	1	102-241

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1525	7tm_1	7 transmembrane receptor (rhodopsin family)	5.6e-14	46.6	1	1-53
1527	Spermine_synth	Spermine/spermidine synthase	6e-13	56.4	1	254-441
1528	efhand	EF hand	3.8e-10	47.1	4	65-91:145-173:329-357:365-393
1530	rvt	Reverse transcriptase	6e-68	239.2	1	125-395
1531	RPH3A_effector	Rabphilin-3A effector domain	1.9e-09	-6.1	1	161-343
1533	TPR	TPR Domain	4.1e-10	47.0	3	220-253:444-477:478-511
1534	SAM	SAM domain (Sterile alpha motif)	0.046	18.0	1	688-752
1538	pkinase	Protein kinase domain	7.2e-42	152.5	2	42-76:82-242
1540	zf-C2H2	Zinc finger, C2H2 type	0.00035	27.3	1	725-750
1541	COLFI	Fibrillar collagen C-terminal domain	8.5e-216	553.4	1	624-841
1542	EGF	EGF-like domain	2.6e-11	51.0	3	916-947:1004-1044:1050-1094
1543	ig	Immunoglobulin domain	1.3e-12	45.7	1	38-112
1544	UCH-1	Ubiquitin carboxyl-terminal hydrolases famil	9.1e-15	62.5	1	477-508
1544	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	6.4e-13	56.3	1	759-811
1544	zf-UBP	Zn-finger in ubiquitin-hydrolases and other	0.00069	18.9	1	350-420
1546	LRR	Leucine Rich Repeat	2.4e-30	114.3	9	132-155:156-179:180-199:201-224:250-269:271-294:295-318:319-341:342-365
1546	LRRNT	Leucine rich repeat N-terminal domain	0.00082	26.1	1	62-84
1551	Peptidase_S9	Prolyl oligopeptidase family	4.3e-10	36.8	1	397-469
1552	Orn_DAP_Arg_d eC	Pyridoxal-dependent decarboxylase, C-	1.5e-14	55.5	1	150-202
1552	Orn_Arg_deC_N	Pyridoxal-dependent decarboxylase, py	4.4e-11	40.3	1	19-117
1555	rvt	Reverse transcriptase	5e-17	67.6	1	616-718
1557	rvt	Reverse transcriptase	1.1e-68	241.6	1	247-520
1558	RhoGEF	RhoGEF domain	1.5e-25	98.4	1	971-1155
1558	PDZ	PDZ domain (Also known as DHR or GLGF)	4.4e-12	53.6	1	159-234
1558	PH	PH domain	0.0017	17.5	1	1199-1312
1559	pkinase	Protein kinase domain	1.9e-24	92.1	2	151-231:309-419
1560	FH2	Formin Homology 2 Domain	4.4e-111	382.4	1	595-1038
1565	HMG_CoA_synt	Hydroxymethylglutaryl-coenzyme A synthas	6.5e-300	1009.7	1	50-582
1568	GCV_H	Glycine cleavage H-protein	1.6e-76	267.6	1	65-185
1577	Peptidase_M1	Peptidase family M1	1.3e-114	332.5	3	42-161:225-354:365-399
1579	rrm	RNA recognition motif	0.0068	23.0	1	823-891
1580	serpin	Serpin (serine protease	8.9e-135	458.1	3	37-241:352-

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
		inhibitor)				475:504-533
1581	CH	Calponin homology (CH) domain	0.012	13.5	1	84-181
1582	LRR	Leucine Rich Repeat	2.2e-37	137.6	12	70-93:94-117:118-141:142-165:166-189:190-213:214-237:238-261:262-285:286-310:311-335:336-359
1582	LRRCT	Leucine rich repeat C-terminal domain	8.1e-12	52.7	1	369-421
1582	ig	Immunoglobulin domain	1.9e-08	32.2	1	438-499
1582	LRRNT	Leucine rich repeat N-terminal domain	0.0099	22.5	1	28-68
1587	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00027	18.1	1	168-213
1587	IBR	IBR domain	0.0071	10.2	1	237-298
1588	rvt	Reverse transcriptase	1.2e-05	25.4	1	192-250
1589	rvt	Reverse transcriptase	1e-10	44.2	1	24-95
1591	TPR	TPR Domain	3.8e-13	57.1	3	254-287:288-321:322-355
1592	PHD	PHD-finger	0.042	2.9	2	684-725:1117-1163
1595	Peptidase_M1	Peptidase family M1	2e-113	329.1	1	100-279
1597	IPPC	Inositol polyphosphate phosphatase family, c	1.1e-15	57.7	1	50-112
1600	thyroglobulin_1	Thyroglobulin type-1 repeat	3.1e-06	34.1	1	38-118
1604	ig	Immunoglobulin domain	0.014	13.3	1	34-59
1606	zf-CXXC	CXXC zinc finger	1.7e-21	84.9	1	50-96
1606	F-box	F-box domain	7.2e-06	32.9	2	545-602:715-762
1606	PHD	PHD-finger	0.062	1.3	1	207-271
1613	rrm	RNA recognition motif	2.9e-14	60.8	1	151-221
1614	SRCR	Scavenger receptor cysteine-rich domain	2.2e-26	101.1	1	52-145
1617	B56	Protein phosphatase 2A regulatory B subunit	6.1e-35	124.7	1	146-218
1618	S1	S1 RNA binding domain	1.2e-10	44.3	1	352-429
1619	trypsin	Trypsin	5.1e-39	125.5	1	30-122
1620	STphosphatase	Ser/Thr protein phosphatase	1.7e-71	245.5	1	66-236
1623	FlgI	Flagellar P-ring protein	5.4e-81	282.5	1	79-231
1623	FlgH	Flagellar L-ring protein	7.5e-34	110.4	1	21-73
1625	Semialdehyde_dh C	Semialdehyde dehydrogenase, dimerisat	8.1e-61	215.5	1	137-308
1625	Semialdehyde_dh	Semialdehyde dehydrogenase, NAD bindi	2.6e-34	109.5	1	20-128
1628	HTH_1	Bacterial regulatory helix-turn-helix protei	2.6e-33	124.1	1	7-146
1631	PEP-utilizers_C	PEP-utilizing enzyme, TIM barrel doma	9.1e-64	225.3	1	53-163
1632	ACR_tran	AcrB/AcrD/AcrF family	3.1e-15	58.8	1	188-254
1632	OTCace	Aspartate/ornithine carbamoyltransferase, A	1.7e-09	35.8	1	459-514
1632	OTCace_N	Aspartate/ornithine carbamoyltransferase, c	0.44	8.5	1	411-426
1632	Replicase	Replicase family	2.9	-	1	399-576

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
				102.2		
1634	ribonuclease_T2	Ribonuclease T2 family	4.3e-17	70.2	1	78-138
1638	efhand	EF hand	5.6e-10	46.6	4	38-66:74-102:111-139:147-175
1638	RrnaAD	Ribosomal RNA adenine dimethylase	5	2.6	1	133-173
1643	Ribosomal_L23	Ribosomal protein L23	1.2e-14	53.9	1	197-276
1645	tsp_1	Thrombospondin type 1 domain	0.0026	21.0	5	420-476:480-534:541-601:607-663:669-718
1647	Arginosuc_synth	Arginosuccinate synthase	2.8e-68	218.8	2	48-126:128-189
1651	vwa	von Willebrand factor type A domain	1.1e-33	125.4	1	89-326
1652	ig	Immunoglobulin domain	6.1e-10	37.1	2	34-117:220-293
1654	PP2C	Protein phosphatase 2C	3.4e-05	21.8	1	86-138
1658	thioredo	Thioredoxin	1.1e-105	354.6	2	324-432:459-570
1662	Hist_deacetyl	Histone deacetylase family	5.5e-85	295.7	2	857-924:1247-1434
1666	wap	WAP-type (Whey Acidic Protein) 'four-disulf	1.5e-21	85.1	1	72-116
1667	KRAB	KRAB box	4.3e-43	156.6	1	106-168
1672	ig	Immunoglobulin domain	1e-13	49.3	3	146-203:245-295:331-402
1674	Transposase_22	L1 transposable element	1.5e-51	184.7	1	6-281
1676	Ribosomal_S2	Ribosomal protein S2	9.5e-09	34.8	1	51-134
1678	ig	Immunoglobulin domain	0.036	12.0	1	35-78
1684	adh_short	short chain dehydrogenase	2.3e-32	120.9	1	2-244
1686	pkinase	Protein kinase domain	2.5e-50	180.6	2	553-770:875-896
1687	HRM	Hormone receptor domain	7.8e-05	29.5	1	82-134
1688	SH3	SH3 domain	1.9e-21	84.7	1	150-206
1688	SH2	SH2 domain	1.2e-08	28.6	1	214-233
1688	RGS	Regulator of G protein signaling domain	0.0003	19.5	1	75-100
1693	LRR	Leucine Rich Repeat	5.3e-34	126.4	10	505-528:529-554:555-573:575-598:613-632:634-657:659-684:686-708:709-732:738-763
1694	SH3	SH3 domain	0.00093	18.2	1	19-73
1701	cystatin	Cystatin domain	8.9e-11	41.4	1	32-78
1705	Ribosomal_S26e	Ribosomal protein S26e	2.1e-16	68.0	1	133-231
1706	ank	Ank repeat	4.9e-30	113.2	3	381-413:414-446:450-482
1706	TPR	TPR Domain	1.4e-06	35.3	4	3-36:43-76:164-197:205-238
1706	LRR	Leucine Rich Repeat	0.0026	24.4	4	716-743:744-764:775-802:835-859
1708	zf-C2H2	Zinc finger, C2H2 type	3.6e-23	90.4	4	51-74:205-227:233-255:261-284
1709	Pep_M12B_prop ep	Reprolysin family propeptide	0.048	-17.2	1	120-196
1710	TIG	IPT/TIG domain	1.4e-101	350.8	10	620-705:708-

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
						788:793-876:883-988:1084-1169:1174-1254:1256-1336:1341-1423:1424-1511:1516-1602
1711	HK	Hydroxyethylthiazole kinase family	5.4e-09	35.0	1	12-39
1711	pp-binding	Phosphopantetheine attachment site	5.4e-09	38.4	1	220-255
1712	IGFBP	Insulin-like growth factor binding pr	2.1e-26	97.4	1	40-99
1712	thyroglobulin_1	Thyroglobulin type-1 repeat	4.6e-05	29.5	1	264-323
1715	rvt	Reverse transcriptase	7.8e-26	99.3	1	18-147
1717	A2M	Alpha-2-macroglobulin family	0	1259.4	4	776-879:880-1111:1112-1172:1243-1530
1717	A2M_N	Alpha-2-macroglobulin family N-terminal regi	0	1092.6	1	75-684
1717	TCPT	Translationally controlled tumor protein	0.0013	-47.0	1	1172-1249
1718	cadherin	Cadherin domain	2e-29	111.2	3	68-159:334-425:439-543
1722	p450	Cytochrome P450	6.3e-48	172.0	1	270-506
1725	ig	Immunoglobulin domain	0.0079	14.2	1	34-116
1726	ig	Immunoglobulin domain	4.2e-05	21.5	2	87-131:145-163
1727	Synaptophysin	Synaptophysin / synaptoporin	2.2e-229	775.4	1	12-307
1729	PA	PA domain	2.4e-29	110.9	1	521-626
1729	Glyco_hydro_47	Glycosyl hydrolase family 47	6.2e-13	28.4	1	99-364
1731	7tm_1	7 transmembrane receptor (rhodopsin family)	1.1e-65	210.8	2	50-117:118-293
1732	ig	Immunoglobulin domain	1.7e-18	64.6	2	49-125:169-239
1734	p450	Cytochrome P450	1e-16	61.8	3	50-106:162-228:298-425
1735	profilin	Profilin	1.5e-15	60.5	1	966-1071
1735	Transposase_22	L1 transposable element	0.00026	-102.7	1	731-1016
1742	PAS	PAS domain	3.2e-07	31.9	3	360-413:474-507:581-613
1744	Dynein_heavy	Dynein heavy chain	9.8e-251	846.4	1	34-781
1745	SCP	SCP-like extracellular protein	9.2e-36	132.2	1	4-180
1749	lipocalin	Lipocalin / cytosolic fatty-acid binding pr	6.5e-05	21.0	1	42-76
1751	SDF	Sodium:dicarboxylate symporter family	1.8e-47	171.2	2	1-34:315-396
1753	ig	Immunoglobulin domain	9.4e-19	65.5	5	49-124:162-219:261-310:345-400:432-496
1753	fn3	Fibronectin type III domain	0.00052	26.8	1	514-606
1757	IPPe	Inositol polyphosphate phosphatase family, c	3e-68	240.1	3	64-350:363-621:753-796

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1762	SSF	Sodium:solute symporter family	4.2e-256	864.2	1	39-477
1763	LRR	Leucine Rich Repeat	3.4e-37	137.0	11	61-84:85-108:109-132:133-156:157-180:181-204:205-228:253-276:277-300:301-324:349-371
1763	ig	Immunoglobulin domain	9.1e-09	33.3	1	428-486
1763	LRRCT	Leucine rich repeat C-terminal domain	3.1e-07	37.5	1	358-411
1763	LRRNT	Leucine rich repeat N-terminal domain	0.00023	27.9	1	30-59
1764	Reprolysin	Reprolysin (M12B) family zinc metalloprote	1.1e-21	85.5	1	156-359
1764	tsp_1	Thrombospondin type 1 domain	2.5e-06	34.5	1	422-491
1768	ANF_receptor	Receptor family ligand binding region	1.9e-34	125.9	1	68-174
1769	C2	C2 domain	2.5e-66	233.8	2	249-337:383-471
1771	cadherin	Cadherin domain	2e-80	280.6	5	140-235:249-343:359-451:465-556:607-697
1775	7tm_1	7 transmembrane receptor (rhodopsin family)	3.2e-34	110.9	2	34-130:147-330
1778	synaptobrevin	Synaptobrevin	2.3e-15	64.5	1	104-192
1780	MHC_I	Class I Histocompatibility antigen, domains	8.1e-93	321.8	1	25-178
1780	ig	Immunoglobulin domain	9.9e-08	30.0	1	194-259
1782	ABC_tran	ABC transporter	7.2e-19	76.1	1	448-626
1783	SNF	Sodium:neurotransmitter symporter family	0	1182.5	1	203-747
1784	TIG	IPT/TIG domain	4.6e-33	123.3	2	1032-1119:1121-1206
1784	Plexin_repeat	Plexin repeat	4.1e-08	40.4	3	653-706:806-858:953-1009
1784	Sema	Sema domain	2.8e-06	26.6	2	59-160:576-602
1785	CTF_NFI	CTF/NF-I family	1.6e-167	570.0	1	651-824
1786	TIR	TIR domain	1e-38	132.4	1	791-931
1786	LRR	Leucine Rich Repeat	4.4e-37	136.6	15	143-166:192-215:216-241:242-266:267-290:385-408:409-432:433-456:457-480:481-502:545-569:570-598:599-622:623-643:645-668
1786	LRRCT	Leucine rich repeat C-terminal domain	7.3e-13	56.2	1	675-726
1788	RPEL	RPEL repeat	1.2e-17	72.1	2	222-247:266-291
1789	ACR_tran	AcrB/AcrD/AcrF family	1.8e-191	649.5	1	1-452
1792	Sulfatase	Sulfatase	0.00013	-44.3	1	502-912
1792	3'5' exonuclease	3'-5' exonuclease	0.0041	-14.7	1	764-923
1794	DUF81	Domain of unknown function DUF81	3.2e-49	176.1	1	8-166

Table 4A

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1796	LRR	Leucine Rich Repeat	7.6e-09	42.8	2	314-337:338-361
1796	LRRCT	Leucine rich repeat C-terminal domain	1.9e-08	41.5	1	371-421
1796	GPS	Latrophilin/CL-1-like GPS domain	0.0041	20.8	1	887-939
1796	HRM	Hormone receptor domain	0.0076	16.3	1	531-600
1796	7tm_2	7 transmembrane receptor (Secretin family)	0.018	- 101.1	1	935-1252
1798	secY	eubacterial secY protein	9.6e-62	218.5	1	1-287
1801	PTR2	POT family	3.5e-38	130.8	2	4-72:364-505
1802	asp	Eukaryotic aspartyl protease	5.1e-13	41.6	1	133-471
1802	Dak1	Dak1 domain	6.7e-06	- 132.2	1	695-1003
1803	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	4.5e-21	83.4	1	4-181
1804	HCO3_cotransp	HCO3- transporter family	1.3e-69	244.7	3	39-52:108-168:171-228
1805	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	5.1e-17	70.0	1	1278-1339
1805	UCH-1	Ubiquitin carboxyl-terminal hydrolases famil	9.3e-08	39.2	1	785-820
1805	zf-UBP	Zn-finger in ubiquitin-hydrolases and other	0.0049	15.8	1	688-727
1806	Nucleoside tran	Nucleoside transporter	5.7e-42	152.8	1	127-446
1810	sugar_tr	Sugar (and other) transporter	0.044	- 132.3	1	637-1048
1813	zf-C2H2	Zinc finger, C2H2 type	1e-38	142.1	7	270-292:298-320:414-437:440-463:485-507:513-535:771-793
1815	trypsin	Trypsin	4.6e-56	179.2	1	28-341
1817	TauD	Taurine catabolism dioxygenase TauD, TfdA fa	1.7e-196	666.2	1	107-385
1818	BPD_transp	Binding-protein-dependent transport system	0.0048	23.3	1	129-194
1819	Y_phosphatase	Protein-tyrosine phosphatase	1.3e-103	357.6	1	1277-1494
1819	fn3	Fibronectin type III domain	1.2e-51	185.1	7	461-541:552-634:641-719:730-812:819-900:908-990:998-1087

Table 4B
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SEQ ID	Model	Description	E-value	Score	Repeats	Position
912	MIF	Macrophage migration inhibitory factor (MIF)	2.4e-54	194.0	1	124-227
912	GST_C	Glutathione S-transferase, C-terminal domain	7.1e-21	82.8	1	410-525
912	GST_N	Glutathione S-transferase, N-terminal domain	2e-15	64.7	1	324-400
913	tsp_1	Thrombospondin type 1 domain	2.9e-23	90.7	2	124-174:181-231
913	EGF	EGF-like domain	1.6e-20	81.6	7	474-508:514-553:559-591:597-633:692-720:802-836:842-882
913	Keratin_B2	Keratin, high sulfur B2 protein	3	-75.8	1	523-649
913	granulin	Granulin	3.2	-15.2	1	484-510
913	TIL	Trypsin Inhibitor like cysteine rich domai	6.4	-13.2	2	540-597:785-842
913	cadherin	Cadherin domain	6.5	-10.4	1	903-995
914	MIF	Macrophage migration inhibitory factor (MIF)	4.5e-50	179.8	1	2-101
915	MIF	Macrophage migration inhibitory factor (MIF)	6.1e-68	239.1	1	2-129
916	trypsin	Trypsin	2.3e-91	316.9	1	445-675
916	kringle	Kringle domain	4.2e-45	163.3	1	286-367
916	fn2	Fibronectin type II domain	4.1e-25	96.9	1	108-148
916	EGF	EGF-like domain	6.2e-15	63.0	2	164-197:245-278
916	fn1	Fibronectin type I domain	4.8e-10	46.8	1	202-237
916	Keratin_B2	Keratin, high sulfur B2 protein	5.3	-79.6	1	104-211
916	DUF32	Domain of unknown function DUF32	9.6	-154.4	1	445-556
917	laminin_EGF	Laminin EGF-like (Domains III and V)	9.8e-159	540.7	12	282-346:349-409:412-469:472-520:523-565:786-831:834-877:880-925:928-984:987-1036:1039-1094:1095-1139
917	laminin_Nterm	Laminin N-terminal (Domain VI)	5.9e-105	362.1	1	45-280
917	DUF26	Domain of unknown function DUF26	3.2	-13.0	1	1110-1155
917	DUF232	Putative transcriptional regulator	3.2	-24.4	1	1149-1281
917	LIM	LIM domain	3.8	-16.6	1	1125-1189
917	zf-CXXC	CXXC zinc finger	4.5	-8.4	1	367-414
917	Methyltransf D12	D12 class N6 adenine-specific DNA met	5.3	-88.8	1	1404-1654
917	VSP	Giardia variant-specific surface prot	8.4	-265.1	1	864-1168
917	EB	EB module	9.5	-12.4	1	1069-1125
918	EGF	EGF-like domain	3.2e-53	190.2	9	33-68:74-110:116-151:161-197:208-243:247-282:288-323:329-362:368-

Table 4B
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SEQ ID	Model	Description	E-value	Score	Repeats	Position
						404
918	CUB	CUB domain	2.9e-17	70.8	1	708-817
918	TIL	Trypsin Inhibitor like cysteine rich domai	1.3	-5.0	1	219-288
918	granulin	Granulin	2.4	-14.4	1	242-284
918	wap	WAP-type (Whey Acidic Protein) 'four-disul	4.7	-8.7	1	6-71
918	Keratin_B2	Keratin, high sulfur B2 protein	6.6	-81.2	1	95-247
918	VSP	Giardia variant-specific surface protein	7.7	-264.1	1	95-403
919	Parathyroid	Parathyroid hormone family	3.1e-82	286.6	1	46-175
920	EGF	EGF-like domain	2.2e-22	87.8	9	2-36:47-82:88-122:128-163:232-263:276-306:319-349:353-394:407-439
921	IL8	Small cytokines (intecrine/chemokine), inter	0.19	-3.2	1	25-65
922	Zn_carbOpept	Zinc carboxypeptidase	8.7e-120	411.4	1	149-429
922	Propep_M14	Carboxypeptidase activation peptide	5.6e-20	79.8	1	7-84
923	fibrinogen_C	Fibrinogen beta and gamma chains, C-term	9.5e-59	208.6	1	62-263
927	FKBP	FKBP-type peptidyl-prolyl cis-trans isomeras	2.4e-41	150.8	1	40-122
930	FAD-oxidase_C	FAD linked oxidases, C-terminal domain	4.1e-88	306.2	1	395-647
930	FAD_binding_4	FAD binding domain	5.2e-78	272.6	2	24-172:219-381
931	UPF0136	Uncharacterised protein family (UPF0136)	0.00031	17.6	1	12-75
933	Fringe	Fringe-like	1.4e-06	-12.8	1	262-487
933	Galactosyl_T	Galactosyltransferase	2.6	-84.8	1	282-439
937	14-3-3	14-3-3 protein	9.5e-124	424.5	1	50-282
938	S_100	S-100/ICaBP type calcium binding domain	3.6e-23	90.4	1	65-108
938	efhand	EF hand	0.0012	25.6	1	114-142
940	ig	Immunoglobulin domain	2.9e-35	130.6	5	38-105:139-206:241-293:326-377:412-487
941	LRR	Leucine Rich Repeat	2e-30	114.5	8	42-63:64-87:88-112:113-136:137-160:161-184:185-208:209-232
941	LRRCT	Leucine rich repeat C-terminal domain	3.6e-07	37.2	1	242-292
941	LRRNT	Leucine rich repeat N-terminal domain	0.46	15.7	1	11-40
944	serpin	Serpin (serine protease inhibitor)	1.6e-133	457.0	1	173-532
947	RUN	RUN domain	8e-44	159.0	1	31-163
947	FYVE	FYVE zinc finger	3.5e-13	57.2	1	529-598
947	Tektin	Tektin family	1.9	-229.2	1	154-473

Table 4B
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SEQ ID	Model	Description	E-value	Score	Repeats	Position
947	filament	Intermediate filament protein	4.7	-202.1	1	216-501
947	PAPS_reduct	Phosphoadenosine phosphosulfate reductase	4.9	-69.1	1	305-467
947	metalthio	Metallothionein	7.3	-11.4	1	576-635
950	lectin_c	Lectin C-type domain	2.4e-08	41.1	1	130-234
951	lectin_c	Lectin C-type domain	8	-36.4	1	215-281
951	FAD-oxidase_C	FAD linked oxidases, C-terminal domain	9.7	-84.1	1	60-267
952	Glyco_transf_8	Glycosyl transferase family 8	0.01	-47.7	1	1255-1526
952	Glyco_hydro_20	Glycosyl hydrolase family 20, catalytic	9.8	-224.0	1	391-674
953	TPR	TPR Domain	0.0042	23.8	1	171-204
954	DENN	DENN (AEX-3) domain	4.2	-67.5	1	16-142
956	Branch	Core-2/I-Branching enzyme	2.2e-77	270.5	1	46-310
957	fn3	Fibronectin type III domain	1.1e-15	65.6	1	30-108
958	Peptidase_M10	Matrixin	5.9e-121	415.2	1	58-225
958	hemopexin	Hemopexin	2e-58	207.5	4	305-347:349-393:398-445:447-487
958	Astacin	Astacin (Peptidase family M12A)	0.28	-108.1	1	128-285
958	PG_binding_1	Putative peptidoglycan binding domain	2.4	-9.5	1	44-112
960	Robl_LC7	Roadblock/LC7 domain	1.8e-30	114.7	1	56-147
962	chromo	'chromo' (Chromatin Organization Modifier)	2.7e-05	31.1	1	47-84
962	SET	SET domain	1.2	-48.2	1	243-307
964	ig	Immunoglobulin domain	0.0047	23.6	1	34-115
967	7tm_1	7 transmembrane receptor (rhodopsin family)	3.5e-13	57.2	1	41-237
968	adh_zinc	Zinc-binding dehydrogenase	2.4e-61	217.2	1	174-495
968	DUF142	Domain of unknown function DUF142	6.6	-67.7	1	248-332
970	E1_dehydrog	Dehydrogenase E1 component	2.1e-183	622.7	1	129-425
970	transketolase	Transketolase, thiamine diphosphate bin	2.6	-227.4	1	173-410
971	ig	Immunoglobulin domain	5.8e-09	43.2	1	45-122
973	zf-MIZ	MIZ zinc finger	3.2e-32	120.5	1	279-331
973	SAP	SAP domain	2.4e-05	31.2	1	2-36
973	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.7	-6.3	1	283-325
975	WD40	WD domain, G-beta repeat	4.3e-09	43.6	3	234-270:446-483:491-528
977	An_peroxidase	Animal haem peroxidase	6.9e-137	468.2	1	137-701
978	Defensin_pro pep	Defensin propeptide	3.8e-19	77.0	1	32-82
978	defensins	Mammalian defensin	0.0015	25.3	1	95-123
981	ig	Immunoglobulin domain	0.00022	28.0	1	49-130
982	ig	Immunoglobulin domain	5.8e-07	36.6	1	36-112
983	Acetyltransf	Acetyltransferase (GNAT)	0.22	15.5	1	260-334

Table 4B
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SEQ ID	Model	Description	E-value	Score	Repeats	Position
		family				
985	tsp_1	Thrombospondin type 1 domain	0.0075	17.1	1	151-206
985	Furin-like	Furin-like cysteine rich region	5.1	-94.5	1	37-149
985	TNFR_c6	TNFR/NGFR cysteine-rich region	9.6	-0.7	1	114-148
987	LRR	Leucine Rich Repeat	5.5e-59	209.4	12	78-101:102-125:126-149:150-173:174-197:198-221:222-245:246-269:270-293:294-317:318-341:342-365
987	LRRNT	Leucine rich repeat N-terminal domain	0.23	18.0	1	24-52
987	Keratin_B2	Keratin, high sulfur B2 protein	6.1	-80.6	1	334-442
988	ParA	ParA family ATPase	0.029	0.0	1	177-283
988	APS_kinase	Adenylylsulfate kinase	0.92	-112.5	1	102-226
988	ArsA_ATPase	Anion-transporting ATPase	0.97	-180.2	1	103-336
989	vwd	von Willebrand factor type D domain	1.1e-38	141.9	1	364-514
989	vwc	von Willebrand factor type C domain	5.3e-35	129.7	5	50-105:108-163:166-224:238-289:301-357
989	TIL	Trypsin Inhibitor like cysteine rich	8.9e-06	32.6	1	629-682
989	Keratin_B2	Keratin, high sulfur B2 protein	1	-68.4	1	264-398
989	TILa	TILa domain	1.4	-2.7	1	301-353
989	fn1	Fibronectin type I domain	2.3	4.7	1	166-198
989	Metallothio_PEC	Plant PEC family metallothionein	4.8	-38.2	1	587-651
990	Cys_knot	Cystine-knot domain	3.2	-31.3	1	227-313
992	ig	Immunoglobulin domain	2.9e-13	57.5	2	34-111:150-220
994	ig	Immunoglobulin domain	1.2e-26	102.0	3	43-110:143-197:230-291
995	SCP	SCP-like extracellular protein	5e-41	149.7	1	4-173
995	granulin	Granulin	6.9	-17.5	1	170-199
996	ig	Immunoglobulin domain	0.014	22.0	1	153-206
999	RNase_PH	3' exoribonuclease family, domain 1	6.1e-23	89.6	1	272-408
999	RNase_PH_C	3' exoribonuclease family, domain 2	1.4e-13	58.5	2	96-157:392-469
999	PNPase	Polyribonucleotide nucleotidyltransferase	8.1e-05	25.9	1	189-269
1000	ig	Immunoglobulin domain	0.00054	26.7	1	38-102
1002	zf-C2H2	Zinc finger, C2H2 type	7.6e-54	192.3	7	183-205:211-233:239-261:267-289:295-317:323-345:351-373
1002	zf-BED	BED zinc finger	3.9	-3.7	1	224-262

Table 4B
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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1002	LIM	LIM domain	7.8	-19.2	1	185-249
1003	zf-C2H2	Zinc finger, C2H2 type	2.3e-114	393.3	16	260-282:297-319:325-347:353-375:381-403:409-431:437-459:465-487:493-515:521-543:549-571:577-599:605-627:633-655:661-683:689-711
1003	zf-BED	BED zinc finger	0.41	5.0	1	366-404
1003	TFIIS	Transcription factor S-II (TFIIS)	0.75	2.4	2	353-391:468-503
1003	GATA	GATA zinc finger	1.8	-6.6	1	435-481
1003	PHD	PHD-finger	5.5	-16.7	1	326-389
1003	E6	Early Protein (E6)	6.9	-67.7	1	467-554
1003	Bowman-Birk leg	Bowman-Birk serine protease inhibitor	8	-18.8	1	355-411
1007	LIM	LIM domain	1.3e-38	141.7	3	390-448:450-507:510-576
1007	E7	E7 protein, Early protein	0.7	-39.5	1	235-422
1008	Transposase_8	Transposase	2.9	-12.7	1	53-148
1010	zf-C2H2	Zinc finger, C2H2 type	4.8e-06	33.5	3	2-24:29-52:154-177
1010	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.1	-7.0	1	4-34
1011	60s_ribosoma1	60s Acidic ribosomal protein	1.2e-20	82.1	1	1-89
1012	abhydrolase_2	Phospholipase/Carboxylesterase	1.3e-24	95.2	1	9-213
1016	Anti_proliferat	BTG1 family	1.7e-73	257.6	1	11-253
1017	zf-C2H2	Zinc finger, C2H2 type	9.8e-71	248.4	11	147-169:213-231:269-291:325-347:353-375:381-403:409-431:437-459:465-487:493-515:521-543
1017	KRAB	KRAB box	2.6e-26	100.8	1	42-82
1017	DM-domain	DM DNA binding domain	0.26	0.8	1	491-539
1017	zf-BED	BED zinc finger	1.8	-0.6	2	338-376:394-432
1017	LIM	LIM domain	3.4	-16.2	1	495-549
1017	zf-TRAF	TRAF-type zinc finger	5	-6.6	1	427-480
1017	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	9.5	-8.1	1	177-218
1017	Bowman-Birk leg	Bowman-Birk serine protease inhibitor	9.6	-19.6	1	147-203
1020	LIM	LIM domain	2.3e-34	127.6	4	78-136:139-197:200-256:259-315
1020	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.3	-4.2	1	106-142
1020	TNFR_c6	TNFR/NGFR cysteine-rich region	8.2	-0.1	1	89-127

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1024	zf-C2H2	Zinc finger, C2H2 type	4.3e-53	189.8	10	156-183:184-206:212-234:240-262:268-290:296-318:324-346:352-374:380-402:408-430
1024	KRAB	KRAB box	2.7e-26	100.8	1	15-55
1024	TFIIS	Transcription factor S-II (TFIIS)	2.5	-2.0	1	129-166
1024	zf-BED	BED zinc finger	3.9	-3.8	1	225-263
1024	fer4	4Fe-4S binding domain	8.3	-3.2	1	176-199
1025	RAG2	Recombination activating protein 2	0	1380.2	1	1-527
1025	PHD	PHD-finger	2.9	-14.2	1	419-483
1026	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-06	35.6	1	16-54
1029	Keratin_B2	Keratin, high sulfur B2 protein	3.8e-06	16.4	2	5-149:150-281
1031	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	4.1e-107	369.3	1	5-165
1035	zf-C2H2	Zinc finger, C2H2 type	1.2e-113	391.0	17	100-122:132-154:160-182:188-210:216-238:244-266:272-294:300-322:328-350:356-378:384-406:412-434:440-462:468-490:496-518:524-546:552-574
1035	KRAB	KRAB box	7.1e-24	92.8	1	4-44
1035	zf-BED	BED zinc finger	0.25	6.9	2	78-123:537-575
1035	LIM	LIM domain	1.5	-13.2	1	330-394
1035	TFIIS	Transcription factor S-II (TFIIS)	2.4	-1.9	1	244-282
1035	zf-MIZ	MIZ zinc finger	8.5	-20.9	1	457-507
1038	Sulfate_transp	Sulfate transporter family	4.3e-103	355.9	2	2-284:441-751
1038	STAS	STAS domain	4.8e-20	80.0	1	774-987
1038	BenE	Benzoate membrane transport protein	1.3	-317.8	1	422-745
1038	UPF0118	Domain of unknown function DUF20	4.9	-125.1	1	454-754
1038	Transp_cyt_pur	Permease for cytosine/purines, uracil	5.3	-195.7	1	403-760
1038	voltage_CLC	Voltage gated chloride channel	5.5	-238.5	1	378-680
1038	FecCD	FecCD transport family	7.9	-219.3	1	440-686
1039	ubiquitin	Ubiquitin family	1.9e-08	41.5	1	55-126
1042	ig	Immunoglobulin domain	3.1e-30	113.9	5	62-129:163-229:264-316:349-400:433-501
1043	UPAR_LY6	u-PAR/Ly-6 domain	7.7e-31	115.9	1	88-158
1044	7tm_5	7TM chemoreceptor	0.17	-139.3	1	29-293
1044	sugar_tr	Sugar (and other) transporter	0.27	-153.3	1	1-419

Table 4B
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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1044	Competence	Competence protein	1.8	-92.8	1	10-207
1044	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	2.6	-160.0	1	185-410
1044	PNTB	NAD(P) transhydrogenase beta subunit	6.6	-392.2	1	188-508
1044	COX1	Cytochrome C and Quinol oxidase polypepti	7.4	-311.2	1	1-396
1045	Lipase_chap	Proteobacterial lipase chaperone prot	3.1	-124.4	1	95-336
1045	Cys_Met_Me ta_PP	Cys/Met metabolism PLP-dependent enzy	8.2	-317.8	1	40-279
1046	PAP2	PAP2 superfamily	7.7	-31.4	1	88-175
1047	MHC_I	Class I Histocompatibility antigen, domains	7.9e-148	504.5	1	25-203
1047	ig	Immunoglobulin domain	0.79	16.0	1	220-285
1050	ig	Immunoglobulin domain	8.7e-07	36.0	1	38-110
1051	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	0.0019	-4.7	1	4-194
1052	GASA	Gibberellin regulated protein	2.6	-47.4	1	1-69
1054	SRCR	Scavenger receptor cysteine-rich domain	6.2e-25	96.3	1	722-820
1055	P2X_receptor	ATP P2X receptor	8.7e-303	1019.3	1	13-388
1055	Metallothio_5	Metallothionein family 5	7.1	-0.8	1	124-161
1057	zona_pellucida	Zona pellucida-like domain	3.1e-81	283.3	1	268-538
1057	trefoil	Trefoil (P-type) domain	0.02	9.1	1	224-262
1058	Aa_trans	Transmembrane amino acid transporter prot	2.4e-22	87.7	1	4-388
1058	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	2.6	-159.9	1	120-362
1058	DUF286	Caenorhabditis protein of unknown functio	2.7	-94.1	1	83-246
1058	Pucc	Pucc protein	8.4	-281.4	1	83-365
1058	Competence	Competence protein	8.4	-105.8	1	99-341
1059	7tm_1	7 transmembrane receptor (rhodopsin family)	1.5e-05	10.6	1	33-401
1060	Na_sulph_sympt	Sodium:sulfate symporter transmembran	4.5e-143	488.7	1	1-554
1060	Na_H_antipor ter	Na ⁺ /H ⁺ antiporter family	5.8	-114.4	1	212-546
1060	LrgA	LrgA family	7.6	-55.7	1	37-141
1061	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	9.5	-171.4	1	129-355
1063	MHC_I	Class I Histocompatibility antigen, domains	9.3e-06	-8.4	1	29-204
1064	ERG4_ERG24	Ergosterol biosynthesis ERG4/ERG24 family	1.1e-103	357.8	1	7-350
1065	Sulfatase	Sulfatase	0.28	-144.2	1	66-431
1065	CRCB	CrcB-like protein	2.6	-51.2	1	728-827
1065	Phosphodiester	Type I phosphodiesterase /	2.7	-167.6	1	43-368

Table 4B
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SEQ ID	Model	Description	E-value	Score	Repeats	Position
		nucleotide p				
1065	Cad	Cadmium resistance transporter	7.5	-136.9	1	412-565
1065	Metalloenzyme	Metalloenzyme superfamily	9.3	-43.8	1	189-308
1066	ig	Immunoglobulin domain	1.2e-15	65.4	3	42-95:135-192:231-288
1067	7tm_1	7 transmembrane receptor (rhodopsin family)	1.5e-28	108.3	1	28-266
1068	UPF0136	Uncharacterised protein family (UPF0136)	4e-45	163.4	1	12-108
1069	pkinase	Protein kinase domain	1.6e-65	231.1	1	298-580
1069	Activin_recp	Activin types I and II receptor domain	6.2e-28	106.2	1	20-107
1069	toxin	Snake toxin	2.8	-19.3	1	33-101
1069	UPAR_LY6	u-PAR/Ly-6 domain	4	-19.7	1	47-101
1070	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	0.00018	13.2	1	3-177
1070	UPF0136	Uncharacterised protein family	3.6	-32.2	1	67-164
1071	MHC_I	Class I Histocompatibility antigen, domains	1.2e-12	55.5	1	24-202
1071	ig	Immunoglobulin domain	3.6e-05	30.6	1	218-284
1072	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	3.1	-60.4	1	36-207
1073	sugar_tr	Sugar (and other) transporter	0.032	-126.5	1	48-528
1073	PUCC	PUCC protein	4.5	-274.8	1	130-432
1073	Competence	Competence protein	6.5	-103.7	1	115-316
1073	Nuc_H_symp ort	Nucleoside H+ symporter	9.6	-276.3	1	72-523
1074	sugar_tr	Sugar (and other) transporter	0.032	-126.5	1	136-616
1074	PUCC	PUCC protein	4.5	-274.8	1	218-520
1074	Competence	Competence protein	6.5	-103.7	1	203-404
1074	Nuc_H_symp ort	Nucleoside H+ symporter	9.6	-276.3	1	160-611
1075	ank	Ankyrin repeat	1.7e-45	164.6	6	31-63:64-96:97-129:130-162:163-195:196-228
1076	7tm_1	7 transmembrane receptor (rhodopsin family)	5.7e-05	-2.6	1	118-374
1076	DUF216	Domain of unknown function DUF	1.6	-42.6	1	193-368
1077	sugar_tr	Sugar (and other) transporter	0.0039	-100.2	1	46-470
1077	OATP_C	Organic Anion Transporter Polypeptide (OATP)	0.018	-180.1	1	64-361
1077	PUCC	PUCC protein	6.2	-278.1	1	85-480
1077	PAP2	PAP2 superfamily	7.9	-31.5	1	353-476
1078	UvrD-helicase	UvrD/REP helicase	7.1	-248.3	1	299-774
1078	DUF246	Plant protein family	9.1	-257.7	1	584-865

Table 4B
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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1079	G_glu_transp ept	Gamma-glutamyltranspeptidase	3.2e-05	-146.3	1	122-499
1079	DLH	Dienelactone hydrolase family	2.5	-92.8	1	189-376
1079	DUF312	Short repeats of unknown function	3.3	0.8	1	415-453
1080	TPR	TPR Domain	2e-19	78.0	5	28-61:68-101:108-141:148-181:188-221
1081	ACAT	Sterol O-acyltransferase	1.9e-32	121.3	1	300-406
1082	WD40	WD domain, G-beta repeat	2.5e-20	81.0	7	1015-1050:1059-1097:1115-1151:1158-1194:1203-1240:1246-1281:1293-1329
1082	V1R	Vomeroneural organ pheromone receptor family	3.2	-162.0	1	421-676
1083	pkinase	Protein kinase domain	1.4e-54	194.8	1	248-568
1083	Activin_rec	Activin types I and II receptor domain	5.8e-38	139.6	1	26-127
1083	UPAR_LY6	u-PAR/Ly-6 domain	7.9	-22.8	1	48-121
1084	pkinase	Protein kinase domain	1.4e-54	194.8	1	310-630
1084	Activin_rec	Activin types I and II receptor domain	5.8e-38	139.6	1	26-127
1084	UPAR_LY6	u-PAR/Ly-6 domain	7.9	-22.8	1	48-121
1086	C2	C2 domain	1.7e-06	35.0	1	233-316
1087	Cache	Cache domain	2.7e-24	94.2	1	557-650
1087	vwa	von Willebrand factor type A domain	0.13	-30.6	1	361-537
1088	Glyco_hydro 31	Glycosyl hydrolases family 31	1.6e-224	759.3	1	1-636
1090	SSrecog	Structure-specific recognition protein	2.7e-153	522.7	1	343-555
1090	HMG_box	HMG (high mobility group) box	3.6e-32	120.3	1	681-749
1090	DUF304	Bacterial membrane flanked domain	4.8	-12.0	1	144-223
1091	serpin	Serpin (serine protease inhibitor)	8.1e-196	663.9	1	315-683
1092	trypsin	Trypsin	0.00023	-4.5	1	334-526
1093	Competence	Competence protein	9.1	-106.5	1	9-260
1094	Aa_trans	Transmembrane amino acid transporter pro	1.5e-07	4.2	1	115-561
1094	Trp_Tyr_per m	Tryptophan/tyrosine permease family	2.7	-283.0	1	118-558
1094	oxidored_q1	NADH-Ubiquinone/plastoquinone	8.1	-170.0	1	117-338
1097	ATP-synt_C	ATP synthase subunit C	3.3e-18	73.9	1	72-140
1098	aconitase	Aconitase family (aconitate hydratase)	1.9e-177	602.9	1	162-744
1098	Aconitase_C	Aconitase C-terminal domain	8.9e-72	251.9	1	872-1043
1103	PAP2	PAP2 superfamily	6.3e-15	63.0	1	89-236
1104	ig	Immunoglobulin domain	1.3e-18	75.3	2	80-148:183-251

Table 4B

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1106	TCTP	Translationally controlled tumor protein	3.5e-93	323.0	1	1-166
1109	efhand	EF hand	1.3e-13	58.7	3	33-61:102-130:138-166
1110	ATP1G1_PL M_MAT8	ATP1G1/PLM/MAT8 family	1.8e-13	58.2	1	92-146
1112	ldl_recept_a	Low-density lipoprotein receptor domain	0.00073	26.3	1	115-153
1112	CUB	CUB domain	0.0032	-3.1	1	9-109
1115	7tm_1	7 transmembrane receptor (rhodopsin family)	1.8e-05	9.0	1	139-349
1116	7tm_1	7 transmembrane receptor	7.5e-21	82.7	1	114-363
1116	oxidored_q5_N	NADH-ubiquinone oxidoreductase chain 4	4.2	-55.0	1	213-282
1116	Abi	CAAX amino terminal protease family	9.4	-28.2	1	171-254
1116	PhaG_MnhG_YufB	Na ⁺ /H ⁺ antiporter subunit	9.8	-57.7	1	281-376
1119	tsp_1	Thrombospondin type 1 domain	4.5e-38	139.9	10	149-198:306-364:571-626:631-696:707-761:841-889:970-1021:1099-1148:1219-1269:1342-1398
1120	HMG14_17	HMG14 and HMG17	1.3e-34	128.4	1	2-86
1124	lectin_c	Lectin C-type domain	5.1	-34.2	1	216-281
1125	ig	Immunoglobulin domain	2.1e-17	71.3	3	84-153:185-255:292-347
1136	sugar_tr	Sugar (and other) transporter	0.029	-125.4	1	23-504
1136	OATP_C	Organic Anion Transporter Polypeptide (OATP)	2.8	-225.4	1	116-381
1136	PUCC	PUCC protein	5.8	-277.4	1	83-476
1136	Frizzled	Frizzled/Smoothed family membrane region	8.3	-247.2	1	54-264
1137	ATP-synt_C	ATP synthase subunit C	3.3e-35	130.4	2	14-79:90-155
1138	DHDPS	Dihydrodipicolinate synthetase family	7.2e-31	116.0	1	34-325
1139	SSF	Sodium:solute symporter family	1.5e-48	174.7	2	50-461:569-953
1139	PNTB	NAD(P) transhydrogenase beta subunit	7.6	-393.3	1	62-347
1139	Competence	Competence protein	8.9	-106.3	1	64-287
1140	Cdc37	Cdc37 family	5.4	-122.6	1	317-539
1143	7tm_1	7 transmembrane receptor (rhodopsin family)	1.3e-44	161.6	1	78-332
1144	Peptidase_A8	Signal peptidase (SPase) II	7.2	-70.3	1	117-211
1145	PID	Phosphotyrosine interaction domain (PTB/PID)	1.7e-99	343.9	2	488-627:661-782
1145	WW	WW domain	1.7e-08	41.7	1	373-401
1145	KdpC	K ⁺ -transporting ATPase, c chain	3.6	-97.4	1	60-245
1146	PRA1	Prenylated rab acceptor (PRA1)	0.0071	-32.6	1	1-153

Table 4B
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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1147	DUF214	Predicted permease	9.5	-68.5	1	17-151
1148	C2	C2 domain	2.1e-30	114.4	2	87-165:240-320
1149	Reticulon	Reticulon	0.29	-68.6	1	65-266
1150	Reticulon	Reticulon	1.8	-81.1	1	79-266
1152	7tm_1	7 transmembrane receptor	2.8e-27	104.1	1	161-410
1152	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	5.3	-166.1	1	90-329
1153	WD40	WD domain, G-beta repeat	9.8e-06	32.5	4	26-62:73-109:236-271:430-467
1155	aa_permeases	Amino acid permease	5.6e-06	-179.9	1	193-613
1155	7tm_5	7TM chemoreceptor	1.6	-156.9	1	199-448
1155	oxidored_q1	NADH-Ubiquinone/plastoquinone	3.7	-162.9	1	306-552
1155	Spore_permease	Spore germination protein	5.6	-193.9	1	180-533
1155	Aa_trans	Transmembrane amino acid transporter p	6.4	-205.1	1	179-589
1155	BPD_transp_2	Branched-chain amino acid transport sy	6.5	-123.5	1	47-327
1157	PRA1	Prenylated rab acceptor (PRA1)	1.1e-46	168.5	1	23-149
1158	dUTPase	dUTPase	5.1e-29	109.8	1	46-167
1158	rvp	Retroviral aspartyl protease	4.1e-22	86.9	1	179-280
1158	G-patch	G-patch domain	0.0011	25.7	1	285-329
1158	MIP	Major intrinsic protein	0.048	-83.0	1	1-111
1159	synaptobrevin	Synaptobrevin	0.49	-3.1	1	96-184
1160	laminin_EGF	Laminin EGF-like (Domains III and V)	9.5e-132	451.1	14	299-353:356-423:426-466:490-532:535-578:584-627:630-680:683-727:1265-1308:1311-1352:1355-1401:1404-1452:1686-1730:1733-1786
1160	laminin_Nterm	Laminin N-terminal (Domain VI)	4e-77	269.6	1	47-297
1160	laminin_G	Laminin G domain	6e-31	116.2	3	2625-2748:3015-3138:3185-3313
1160	laminin_B	Laminin B (Domain IV)	1.1e-09	45.6	1	1517-1651
1160	MCPsignal	Methyl-accepting chemotaxis protein	0.61	-119.3	1	2011-2237
1160	TSPN	Thrombospondin N-terminal -like domain	1.7	-47.9	1	3143-3311
1160	filament	Intermediate filament protein	2.2	-193.4	1	1826-2081
1160	DSL	Delta serrate ligand	3.3	-17.5	1	472-519
1160	OEP	Outer membrane efflux protein	3.7	-29.3	1	2020-2211
1160	EB	EB module	6.5	-10.6	1	665-713
1160	Apidaecin	Apidaecin	7	7.3	1	907-934
1160	Acetate_kinase	Acetokinase family	8.3	-242.2	1	2093-2412

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1160	spectrin	Spectrin repeat	8.4	-20.0	1	2105-2205
1161	EGF	EGF-like domain	2.2e-26	101.1	5	29-57:60-88:104-140:147-178:185-216
1161	EB	EB module	1.7	-4.2	1	131-178
1161	metalthio	Metallothionein	7.7	-11.7	1	64-133
1162	interferon	Interferon alpha/beta domain	1.5e-17	71.7	1	16-171
1163	IL1	Interleukin-1 / 18	8.7e-21	82.5	1	19-159
1164	PDGF	Platelet-derived growth factor (PDGF)	1.8e-51	184.4	1	52-130
1165	IL1	Interleukin-1 / 18	3.7e-23	90.4	1	11-144
1167	Palmitoest	Palmitoyl protein thioesterase	2.4e-216	732.1	1	28-282
1168	serpin	Serpin (serine protease inhibitor)	1.6e-202	686.2	1	47-415
1170	Defensin_pro pep	Defensin propeptide	1.2e-26	102.0	1	38-90
1170	defensins	Mammalian defensin	7.3e-14	59.5	1	103-131
1172	Y_phosphatase	Protein-tyrosine phosphatase	1.8e-110	380.4	1	271-499
1179	Metallophos	Calcineurin-like phosphoesterase	1.1e-11	52.3	1	70-285
1184	MHC_I	Class I Histocompatibility antigen, domains	6.2e-06	-5.9	1	29-205
1187	PLA2_B	Lysophospholipase catalytic domain	8.3e-53	188.9	1	357-800
1187	C2	C2 domain	1.6e-06	35.1	1	46-129
1189	lipocalin	Lipocalin / cytosolic fatty-acid binding	2.6e-39	144.0	1	39-188
1189	Kunitz_BPTI	Kunitz/Bovine pancreatic trypsin inhibitor	4.7e-23	90.0	2	231-273:274-319
1190	ig	Immunoglobulin domain	4e-07	37.1	1	38-116
1191	ig	Immunoglobulin domain	4e-07	37.1	1	38-116
1196	UPF0185	Uncharacterised protein family (UPF0185)	3.6e-41	150.2	1	15-102
1200	zf-DHHC	DHHC zinc finger domain	3.7e-15	63.8	1	87-149
1201	KRAB	KRAB box	6.6e-22	86.2	1	33-73
1202	KRAB	KRAB box	6.6e-22	86.2	1	33-73
1204	trypsin	Trypsin	3e-31	117.2	1	56-239
1208	lipocalin	Lipocalin / cytosolic fatty-acid binding pr	0.12	9.2	1	38-186
1212	LRR	Leucine Rich Repeat	2.5e-54	193.9	15	73-96:97-122:123-149:150-175:176-195:197-220:221-246:247-270:292-317:318-337:339-362:363-388:389-408:410-433:434-459
1212	LRRNT	Leucine rich repeat N-terminal domain	0.24	17.9	1	43-71
1212	SCAN	SCAN domain	7.2	-38.8	1	88-187
1213	Zn_carboxypeptidase	Zinc carboxypeptidase	1.9e-61	217.6	1	50-285

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1214	ig	Immunoglobulin domain	5.5	9.1	1	17-84
1216	death	Death domain	2.4	-0.1	1	93-180
1217	death	Death domain	1.5	2.0	1	73-160
1221	C1q	C1q domain	3.4e-41	150.3	1	134-258
1221	Collagen	Collagen triple helix repeat (20 copies)	2.6e-10	47.7	1	41-100
1223	pkinase	Protein kinase domain	9e-75	261.8	1	158-417
1223	SH3	SH3 domain	0.019	7.4	1	423-478
1223	UBA	UBA/TS-N domain	0.035	20.7	1	987-1026
1224	vwa	von Willebrand factor type A domain	1.2e-05	29.0	1	51-242
1225	abhydrolase	alpha/beta hydrolase fold	3.7e-12	53.8	1	111-390
1225	abhydrolase_2	Phospholipase/Carboxylesterase	2.3	-88.8	1	64-270
1227	lectin_c	Lectin C-type domain	9.6e-29	108.9	1	54-166
1237	fibrinogen_C	Fibrinogen beta and gamma chains, C-term	1.5e-09	-1.3	1	242-385
1257	LRR	Leucine Rich Repeat	9e-65	228.6	14	78-101:102-125:126-149:150-173:174-197:198-221:222-245:246-269:270-293:294-317:318-341:342-365:366-389:390-413
1257	LRRCT	Leucine rich repeat C-terminal domain	0.011	22.3	1	423-475
1257	LRRNT	Leucine rich repeat N-terminal domain	0.23	18.0	1	24-52
1263	Pep_M12B_p ropep	Reprolysin family propeptide	1.8e-28	108.1	1	75-191
1263	disintegrin	Disintegrin	2.7e-11	51.0	1	419-494
1263	Reprolysin	Reprolysin (M12B) family zinc metallo	7.3e-07	-22.2	1	206-402
1263	EGF	EGF-like domain	2.7	10.3	1	635-663
1266	Clusterin	Clusterin	2.3e-298	1004.6	1	2-394
1267	serpin	Serpin (serine protease inhibitor)	3.8e-140	479.0	1	80-425
1268	serpin	Serpin (serine protease inhibitor)	6.8e-162	551.2	1	98-461
1269	COX6C	Cytochrome c oxidase subunit VIc	2.3e-38	140.9	1	1-75
1270	Cadherin_C_t erm	Cadherin cytoplasmic region	4	-79.4	1	13-130
1271	spectrin	Spectrin repeat	8.2	-19.9	1	307-417
1272	W2	eIF4-gamma/eIF5/eIF2-epsilon	7.3	-26.9	1	325-395
1272	spectrin	Spectrin repeat	8.3	-19.9	1	327-437
1273	Rhodanese	Rhodanese-like domain	1.5e-48	174.7	2	16-138:165-266
1274	trypsin	Trypsin	2.9e-80	280.1	1	121-346
1279	Calpain_III	Calpain large subunit, domain III	1.5e-25	98.3	1	30-179
1284	Ribosomal_L 35p	Ribosomal protein L35	2.4	-18.1	1	122-179
1285	Ribosomal_L	Ribosomal protein L35	2.4	-18.1	1	122-179

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
	35p					
1287	zf-C2H2	Zinc finger, C2H2 type	4.4e-66	233.0	9	173-195:201-223:229-251:257-279:285-307:313-335:341-363:369-391:397-419
1287	KRAB	KRAB box	4.9e-23	90.0	1	14-54
1287	zf-BED	BED zinc finger	2.4	-1.9	1	186-224
1287	LIM	LIM domain	9.3	-19.9	1	175-239
1292	EGF	EGF-like domain	0.36	17.3	1	30-65
1294	vwc	von Willebrand factor type C domain	1.3e-09	45.4	1	69-127
1295	zf-C2H2	Zinc finger, C2H2 type	5e-50	179.6	8	263-285:319-341:347-369:375-397:403-425:431-453:459-481:487-510
1295	KRAB	KRAB box	8.9e-26	99.1	1	8-48
1295	TFIIS	Transcription factor S-II (TFIIS)	5.7	-5.0	1	431-469
1295	zf-TRAF	TRAF-type zinc finger	7.3	-8.4	1	369-419
1295	LIM	LIM domain	7.7	-19.2	1	321-385
1296	zf-C2H2	Zinc finger, C2H2 type	3.2e-113	389.6	13	190-212:218-240:246-268:274-296:302-324:330-352:358-380:386-408:414-436:442-464:470-492:498-520:526-548
1296	KRAB	KRAB box	6.7e-28	106.1	1	14-54
1296	zf-BED	BED zinc finger	0.51	4.1	1	511-549
1296	PHD	PHD-finger	2.4	-13.4	1	275-338
1296	TFIIS	Transcription factor S-II (TFIIS)	7.6	-6.1	1	330-368
1296	LIM	LIM domain	8.1	-19.4	1	388-456
1299	hemopexin	Hemopexin	7e-25	96.1	4	279-322:324-367:369-415:417-461
1299	Peptidase_M10	Matrixin	8.4e-14	58.8	1	1-176
1299	Astacin	Astacin (Peptidase family M12A)	1.4	-117.0	1	91-238
1301	ig	Immunoglobulin domain	0.67	16.4	1	33-116
1305	DUF25	Domain of unknown function DUF25	5.3e-76	265.9	1	40-162
1307	kazal	Kazal-type serine protease inhibitor domain	1.3e-12	55.3	1	21-68
1309	Defensin_pro pep	Defensin propeptide	1.2e-26	102.0	1	74-126
1309	defensins	Mammalian defensin	7.3e-14	59.5	1	139-167
1312	ras	Ras family	2.7e-59	210.4	1	64-253
1312	GTP_EFTU	Elongation factor Tu GTP binding domain	0.91	-79.4	1	61-226
1312	arf	ADP-ribosylation factor family	4.3	-116.7	1	46-226

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1314	zf-C2H2	Zinc finger, C2H2 type	1.1e-51	185.1	8	163-185:191-213:219-241:247-269:275-297:303-325:331-353:359-381
1314	LIM	LIM domain	1.8	-13.9	1	221-285
1314	PHD	PHD-finger	2.5	-13.5	1	304-367
1314	zf-BED	BED zinc finger	2.8	-2.4	1	232-270
1315	Keratin_B2	Keratin, high sulfur B2 protein	0.0035	-30.0	1	13-154
1316	Keratin_B2	Keratin, high sulfur B2 protein	3.6e-15	63.8	1	23-154
1317	Keratin_B2	Keratin, high sulfur B2 protein	8.2e-20	79.2	2	20-163:164-295
1318	Keratin_B2	Keratin, high sulfur B2 protein	5.5	-79.9	1	3-172
1319	zf-C2H2	Zinc finger, C2H2 type	2.9e-52	187.1	7	33-55:61-83:89-111:117-139:145-167:173-195:201-223
1319	PHD	PHD-finger	1.6	-11.8	1	146-209
1319	zf-BED	BED zinc finger	3.4	-3.2	1	74-112
1321	Keratin_B2	Keratin, high sulfur B2 protein	0.00014	-8.3	1	23-193
1331	ig	Immunoglobulin domain	9.7e-06	32.5	1	24-78
1332	Kunitz_BPT1	Kunitz/Bovine pancreatic trypsin inhibito	2.2e-18	74.5	1	76-126
1333	zf-C2H2	Zinc finger, C2H2 type	4.6e-55	196.3	7	199-221:227-249:255-277:283-305:311-333:339-361:367-389
1333	KRAB	KRAB box	5.8e-24	93.0	1	6-46
1333	zf-BED	BED zinc finger	0.31	6.1	2	240-278:352-390
1336	vwa	von Willebrand factor type A domain	0.0038	-8.1	1	32-193
1336	TIG	IPT/TIG domain	1.4	4.5	1	199-291
1337	vwa	von Willebrand factor type A domain	0.0038	-8.1	1	32-193
1337	TIG	IPT/TIG domain	1.4	4.5	1	199-291
1339	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	0.0088	-16.3	1	4-203
1340	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	0.0019	-4.7	1	4-194
1341	PsaL	Photosystem I reaction centre subunit XI	4.6	-111.8	1	21-106
1343	ig	Immunoglobulin domain	1.5e-13	58.5	2	81-158:204-278
1344	MARCKS	MARCKS family	6.7	-95.4	1	124-395
1347	ig	Immunoglobulin domain	1.2e-07	38.9	2	168-226:276-330
1348	ig	Immunoglobulin domain	1.5e-18	75.1	3	157-217:269-325:373-427
1348	rhv	picornavirus capsid protein	1.4	-52.0	1	28-258
1353	LRR	Leucine Rich Repeat	2e-39	144.4	9	120-143:144-167:168-191:192-

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
						215:216-239:240-263:264-287:311-334:335-358
1353	LRRNT	Leucine rich repeat N-terminal domain	0.0066	23.1	1	92-119
1353	LRRCT	Leucine rich repeat C-terminal domain	1.5	4.9	1	368-418
1353	Bgal_small_C	Beta galactosidase small chain, C termin	6.6	-44.4	1	105-174
1354	oxidored_q4	NADH-ubiquinone/plastoquinone oxidoreduct	5.8	-35.2	1	60-142
1356	ig	Immunoglobulin domain	2.1e-17	71.3	3	37-106:138-208:245-300
1357	CD36	CD36 family	3.9e-231	781.3	1	5-445
1358	DUF139	Cysteine rich repeat (DUF139)	1.2e-08	42.2	4	195-211:245-261:288-304:316-332
1359	ig	Immunoglobulin domain	1.6e-06	35.1	2	41-124:156-230
1359	Gag_MA	Matrix protein (MA), p15	0.0044	-25.2	1	291-429
1360	ion_trans	Ion transport protein	0.0031	24.2	1	285-445
1360	DUF214	Predicted permease	8.6	-67.8	1	202-378
1363	spectrin	Spectrin repeat	9.5e-22	85.7	6	17-121:124-226:229-340:372-476:678-785:788-896
1363	Remorin_C	Remorin, C-terminal region	3.5	-39.8	1	659-744
1366	C1q	C1q domain	2.1e-31	117.8	1	266-390
1366	Collagen	Collagen triple helix repeat (20 copies)	0.00029	19.8	1	182-241
1367	rnaseA	Pancreatic ribonuclease	1.1e-34	128.7	1	27-132
1368	3HCDH_N	3-hydroxyacyl-CoA dehydrogenase, NAD binding	0.0021	-60.2	1	50-141
1369	3HCDH_N	3-hydroxyacyl-CoA dehydrogenase, NAD binding	0.25	-91.5	1	50-153
1371	voltage_CLC	Voltage gated chloride channel	3.1e-199	675.3	1	92-528
1371	CBS	CBS domain	4.9e-16	66.7	2	559-617:761-814
1371	PHO4	Phosphate transporter family	4.1	-199.1	1	129-495
1371	K_trans	K ⁺ potassium transporter	5.8	-566.6	1	267-759
1371	7tm_5	7TM chemoreceptor	6.3	-167.6	1	254-486
1372	7tm_1	7 transmembrane receptor (rhodopsin family)	0.2	-84.7	1	82-199
1373	ldh_C	lactate/malate dehydrogenase, alpha/beta C-t	0.69	-61.5	1	38-200
1374	disintegrin	Disintegrin	7.2	-30.4	1	241-306
1375	Peptidase_C1	Papain family cysteine protease	1e-120	414.5	1	114-332
1376	7tm_1	7 transmembrane receptor	2.6e-50	180.6	1	48-454
1376	7tm_5	7TM chemoreceptor	1	-153.3	1	26-453
1376	Sec62	Translocation protein Sec62	1.4	-124.2	1	307-477

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1376	DUF280	Caenorhabditis protein of unknown function	5.6	-141.0	1	93-274
1376	Sre	C. elegans Sre G protein-coupled chemoreceptor	7.2	-136.9	1	1-503
1376	Colicin_im	Colicin immunity protein	9.6	-61.3	1	365-466
1378	7tm_2	7 transmembrane receptor (Secretin family)	4.9e-09	32.5	1	250-500
1378	GPS	Latrophilin/CL-1-like GPS domain	0.38	4.4	1	197-248
1378	Competence	Competence protein	5.9	-102.8	1	240-490
1380	MAGE	MAGE family	1.4e-91	317.7	1	3-231
1381	ion_trans	Ion transport protein	0.065	16.8	1	158-323
1381	ABC2_membrane	ABC-2 type transporter	6.1	-130.1	1	150-339
1381	oxidored_q1	NADH-Ubiquinone/plastoquinone	6.2	-167.5	1	51-322
1381	OATP_C	Organic Anion Transporter Polypeptide	9.5	-236.4	1	80-321
1382	ig	Immunoglobulin domain	7e-12	52.9	2	37-128:160-241
1385	MHC_I	Class I Histocompatibility antigen, domains	9.3e-06	-8.4	1	29-204
1388	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	7e-88	305.4	1	45-184
1390	7tm_1	7 transmembrane receptor (rhodopsin family)	5.3e-06	21.2	1	1-210
1391	Reticulon	Reticulon	6.4	-89.9	1	52-257
1392	Collagen	Collagen triple helix repeat	0.92	-48.2	1	27-84
1392	MDM2	p53-associated protein (MDM2)	5.1	-12.8	1	92-155
1392	Cytidyltrans	Phosphatidate cytidyltransferase	9.4	-91.4	1	141-242
1393	7tm_1	7 transmembrane receptor (rhodopsin family)	1.6e-12	55.0	1	99-329
1393	DUF40	Domain of unknown function DUF40	5.7	-131.9	1	97-267
1395	trefoil	Trefoil (P-type) domain	3.9	-11.1	1	28-53
1397	fn3	Fibronectin type III domain	4.7e-78	272.7	5	533-619:631-717:734-833:854-939:951-1039
1397	ig	Immunoglobulin domain	3.7e-42	153.5	5	154-227:261-318:362-418:453-511:1253-1316
1398	DUF300	Domain of unknown function	1.4e-152	520.3	1	51-341
1404	ig	Immunoglobulin domain	2.9e-08	40.9	2	42-99:139-198
1409	ig	Immunoglobulin domain	8.1e-30	112.5	3	142-199:263-321:359-438
1410	Tissue_fac	Tissue factor	0.26	-135.2	1	1-267
1410	HRM	Hormone receptor domain	8.4	-13.9	1	28-101
1412	FecCD	FecCD transport family	7.2	-218.5	1	144-342
1413	Metallothio_P	Prokaryotic metallothionein	6.2	-8.0	1	464-511
1414	mito_carr	Mitochondrial carrier protein	3.5e-64	226.7	3	40-130:137-227:238-322
1416	ig	Immunoglobulin domain	0.0011	25.6	1	57-112

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1417	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	6.6e-06	33.1	1	27-67
1418	Synaptophysin	Synaptophysin / synaptoporin	6.9e-71	248.9	1	27-272
1419	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	5.2e-18	73.3	1	4-165
1421	Ammonium_transporter	Ammonium Transporter Family	8.5e-18	72.6	1	25-383
1421	FecCD	FecCD transport family	1.8	-206.7	1	97-311
1421	Bac_chlorC	Bacteriochlorophyll C binding protein	5.8	-12.0	1	212-289
1423	rnaseA	Pancreatic ribonuclease	4.1e-29	110.1	1	32-136
1424	PCI	PCI domain	8.5	-9.1	1	64-133
1424	Nrap	Nrap protein	9.7	-257.5	1	162-764
1425	CbiM	CbiM	3.4	-86.8	1	16-138
1427	LRR	Leucine Rich Repeat	4.5e-26	100.0	6	3-26:27-50:51-74:76-99:100-123:124-144
1427	fn3	Fibronectin type III domain	2.7e-08	41.0	1	334-417
1427	ig	Immunoglobulin domain	2.4e-07	37.9	1	225-283
1427	LRRCT	Leucine rich repeat C-terminal domain	7.2e-06	32.9	1	164-209
1428	GRAM	GRAM domain	0.067	13.1	1	177-245
1429	YGGT	YGGT family	7.4	-24.4	1	147-217
1431	Papilloma_E5	Papillomavirus E5	6.7	-34.9	1	52-108
1435	Rhomboid	Rhomboid family	1.5e-45	164.8	1	169-326
1435	efhand	EF hand	3.8	11.0	1	38-66
1437	Sema	Sema domain	7e-202	684.1	1	102-513
1437	tsp_1	Thrombospondin type 1 domain	1.1e-42	155.3	6	589-637:644-695:702-746:833-883:890-940:945-985
1437	PSI	Plexin repeat	2.5e-14	61.0	1	531-578
1438	ank	Ankyrin repeat	2e-15	64.7	3	336-368:383-418:468-498
1438	ion_trans	Ion transport protein	9.4e-07	35.9	1	615-817
1439	ank	Ankyrin repeat	3.3e-12	54.0	3	417-449:464-499:549-579
1439	ion_trans	Ion transport protein	9.4e-07	35.9	1	696-898
1442	LRR	Leucine Rich Repeat	3.2e-20	80.6	5	57-80:81-104:105-128:129-152:153-176
1442	LRRCT	Leucine rich repeat C-terminal domain	2.3e-07	37.9	1	186-240
1442	LRRNT	Leucine rich repeat N-terminal domain	0.00013	28.8	1	27-55
1443	7tm_2	7 transmembrane receptor (Secretin family)	7.2e-23	89.4	1	166-476
1443	HMG_box	HMG (high mobility group) box	3.1e-05	30.8	1	3-76
1443	GPS	Latrophilin/CL-1-like GPS domain	0.0066	19.1	1	110-162
1443	7tm_1	7 transmembrane receptor (rhodopsin family)	1.9	-107.5	1	255-473

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1443	Frizzled	Frizzled/Smoothed family membrane region	3.3	-241.3	1	156-459
1444	DUF214	Predicted permease	0.0051	-16.4	1	136-275
1444	secY	eubacterial secY protein	1.1	-230.8	1	13-270
1448	ribonuc_red_s m	Ribonucleotide reductase, small chain	5.6	-142.1	1	529-805
1452	mito_carr	Mitochondrial carrier protein	8.4e-58	205.5	2	27-123:124-217
1454	mito_carr	Mitochondrial carrier protein	0.00049	22.3	2	79-179:198-287
1455	WD40	WD domain, G-beta repeat	2.7e-26	100.8	4	64-99:105-141:235-273:279-315
1456	Furin-like	Furin-like cysteine rich region	6.1e-89	308.9	1	172-328
1456	Recep_L_do main	Receptor L domain	3.1e-80	280.0	2	46-169:345-471
1456	pkinase	Protein kinase domain	7e-65	229.0	1	986-1258
1456	fn3	Fibronectin type III domain	0.2	11.5	2	604-794:814-909
1456	fer4	4Fe-4S binding domain	3.7	-1.0	1	238-267
1456	Keratin_B2	Keratin, high sulfur B2 protein	5.2	-79.5	1	143-285
1456	TIL	Trypsin Inhibitor like cysteine rich d	6.3	-13.2	1	221-279
1462	Peptidase_M1 0	Matrixin	1.5e-79	277.7	1	62-227
1462	hemopexin	Hemopexin	1.4e-10	48.6	1	309-350
1463	Armadillo_se g	Armadillo/beta-catenin-like repeat	0.028	21.0	4	549-591:641-685:686-737:738-783
1466	C2	C2 domain	6.5e-07	36.4	1	219-304
1468	RTC	RNA 3'-terminal phosphate cyclase	6.1e-05	-118.8	1	9-196
1476	CN_hydrolas e	Carbon-nitrogen hydrolase	0.0014	-76.2	1	64-341
1477	zf-C2H2	Zinc finger, C2H2 type	4.8e-06	33.5	3	267-289:294-317:419-442
1477	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.1	-7.0	1	269-299
1478	Euk_porin	Eukaryotic porin	3.3e-06	-42.1	1	1-142
1482	ras	Ras family	0.24	-121.5	1	389-513
1484	BTB	BTB/POZ domain	2.3e-13	57.8	1	88-194
1487	rvt	Reverse transcriptase	8.1e-57	202.2	1	241-507
1489	Galactosyl_T 2	Galactosyltransferase	4.7e-177	601.6	1	97-404
1489	TT_ORF2	TT viral ORF2	9	-98.0	1	339-453
1490	Orexin	Prepro-orexin	8.3	-32.3	1	1-128
1491	GBP_C	Guanylate-binding protein, C-terminal domain	0.00059	-84.4	1	2-155
1493	NUDIX	NUDIX domain	0.0011	21.7	1	297-439
1496	Big_2	Bacterial Ig-like domain (group 2)	4.5e-16	66.8	1	1177-1258
1497	ig	Immunoglobulin domain	1.9e-10	48.2	1	38-112
1498	aldo_ket_red	Aldo/keto reductase family	3.7e-08	-8.7	1	108-367
1502	Caveolin	Caveolin	1.6e-06	13.3	1	90-262

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1504	sushi	Sushi domain (SCR repeat)	8.2e-16	66.0	2	223-281:286-344
1511	zf-C2H2	Zinc finger, C2H2 type	1.1e-16	68.9	2	341-363:369-391
1511	KRAB	KRAB box	4.9e-09	43.5	1	230-268
1511	zf-BED	BED zinc finger	4.1	-3.9	1	354-392
1516	CBS	CBS domain	1.4e-30	115.0	3	189-243:264-317:336-389
1517	zf-C2H2	Zinc finger, C2H2 type	2.4e-128	439.8	18	279-301:307-329:335-357:363-385:391-413:419-441:447-469:475-497:503-525:868-890:896-918:924-946:952-974:980-1002:1008-1030:1036-1058:1064-1086:1092-1114
1517	KRAB	KRAB box	5.6e-40	146.2	2	74-114:681-713
1517	PHD	PHD-finger	1.2	-10.7	1	897-960
1517	SCAN	SCAN domain	1.6	-32.1	1	544-624
1517	LIM	LIM domain	5.4	-17.9	1	337-401
1517	BolA	BolA-like protein	6.1	-25.1	1	283-347
1517	TFIIS	Transcription factor S-II (TFIIS)	9.1	-6.8	1	952-990
1518	ig	Immunoglobulin domain	1e-06	35.7	1	38-102
1521	CoA_trans	Coenzyme A transferase	1.1e-161	550.5	2	42-261:271-472
1521	TGF-beta	Transforming growth factor beta like domain	6.8e-64	225.7	1	637-741
1523	Reprolysin	Reprolysin (M12B) family zinc metallo	6.6e-95	328.7	1	223-422
1523	Pep_M12B_p ropep	Reprolysin family propeptide	2e-27	104.5	1	121-248
1523	disintegrin	Disintegrin	1.9e-14	61.5	1	437-513
1523	EGF	EGF-like domain	0.0092	22.6	1	661-693
1523	VSP	Giardia variant-specific surface prot	4.9	-258.5	1	428-750
1523	Keratin_B2	Keratin, high sulfur B2 protein	7.2	-81.7	1	427-538
1524	DSPc	Dual specificity phosphatase, catalytic doma	3.6e-71	249.9	1	102-241
1527	Spermine_syn th	Spermine/spermidine synthase	8.2e-13	56.0	1	254-440
1528	efhand	EF hand	3.4e-10	47.3	4	65-91:145-173:329-357:365-393
1529	Epimerase	NAD dependent epimerase/dehydratase family	0.66	-192.0	1	10-451
1530	rvt	Reverse transcriptase	7.7e-69	242.1	1	125-395
1531	RPH3A_effec tor	Rabphilin-3A effector domain	1.9e-09	-6.1	1	161-339
1533	TPR	TPR Domain	3.7e-10	47.2	3	220-253:444-477:478-511
1533	CENP-B	CENP-B protein	1.2e-06	-7.7	1	541-671
1534	SAM	SAM domain (Sterile alpha	0.045	18.0	1	688-752

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
		motif)				
1534	Atrophin-1	Atrophin-1 family	7.9	-679.9	1	731-1402
1538	pkinese	Protein kinase domain	1.5e-20	81.7	1	42-242
1540	zf-C2H2	Zinc finger, C2H2 type	0.00035	27.3	1	725-750
1541	COLFI	Fibrillar collagen C-terminal domain	3.9e-163	555.3	1	624-841
1541	Collagen	Collagen triple helix repeat (20 copies)	2.2	-55.6	1	538-597
1541	TT ORF2	TT viral ORF2	3.9	-93.3	1	508-610
1542	EGF	EGF-like domain	2.6e-11	51.0	3	916-947:1004-1044:1050-1094
1542	granulin	Granulin	6.3	-17.2	1	1019-1074
1542	TIL	Trypsin Inhibitor like cysteine rich domain	9.4	-15.2	1	938-1004
1543	ig	Immunoglobulin domain	1.5e-10	48.5	1	38-112
1544	UCH-1	Ubiquitin carboxyl-terminal hydrolases famil	8.5e-15	62.6	1	477-508
1544	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	7.3e-13	56.2	1	759-811
1544	zf-UBP	Zn-finger in ubiquitin-hydrolases and other	0.011	20.7	1	350-420
1545	spectrin	Spectrin repeat	2.8	-14.5	1	696-803
1546	LRR	Leucine Rich Repeat	1.1e-30	115.3	9	132-155:156-179:180-199:201-224:250-269:271-294:295-318:319-341:342-365
1546	LRRNT	Leucine rich repeat N-terminal domain	0.00082	26.1	1	62-84
1547	Allantoicase	Allantoicase repeat	7e-70	245.6	2	116-271:376-476
1547	DCX	Doublecortin	3.3e-17	70.6	1	611-671
1551	Peptidase_S9	Prolyl oligopeptidase family	1.7e-06	35.0	1	389-469
1551	DPPIV_N_term	Dipeptidyl peptidase IV (DPP IV) N-termi	1.4	-267.4	1	1-385
1551	DLH	Dienelactone hydrolase family	4.7	-96.4	1	355-597
1552	Orn_DAP_Ar g_deC	Pyridoxal-dependent decarboxylase, C-	1.3e-05	23.1	1	84-202
1555	rvt	Reverse transcriptase	0.00015	7.9	1	505-718
1557	rvt	Reverse transcriptase	1.4e-69	244.6	1	247-520
1557	RcbX	RcbX protein	1.8	-79.3	1	1-108
1558	RhoGEF	RhoGEF domain	9.1e-26	99.0	1	971-1155
1558	PDZ	PDZ domain (Also known as DHR or GLGF)	4.2e-12	53.6	1	159-234
1558	PH	PH domain	0.081	19.5	1	1199-1312
1558	RGS	Regulator of G protein signaling domain	2.5	-34.3	1	465-577
1559	pkinese	Protein kinase domain	9e-11	20.4	1	151-443
1560	FH2	Formin Homology 2 Domain	4e-105	362.7	1	595-1038
1561	Keratin_B2	Keratin, high sulfur B2 protein	9.6	-83.6	1	136-235
1565	HMG_CoA_synt	Hydroxymethylglutaryl-coenzyme A synthas	6.5e-300	1009.7	1	50-582
1568	GCV_H	Glycine cleavage H-protein	4.3e-77	269.5	1	65-185

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1570	DLH	Dienelactone hydrolase family	0.039	-69.3	1	168-431
1577	Peptidase_M1	Peptidase family M1	5.6e-74	259.2	1	42-399
1577	DUF59	Domain of unknown function DUF59	1.8	-24.4	1	188-265
1579	rrm	RNA recognition motif.	0.0082	22.8	1	823-891
1579	zf-C2H2	Zinc finger, C2H2 type	9.5	9.5	1	584-608
1580	serpin	Serpin (serine protease inhibitor)	2.1e-107	370.3	1	37-541
1581	CH	Calponin homology (CH) domain	0.012	13.5	1	84-181
1582	LRR	Leucine Rich Repeat	9.6e-38	138.8	12	70-93:94-117:118-141:142-165:166-189:190-213:214-237:238-261:262-285:286-310:311-335:336-359
1582	LRRCT	Leucine rich repeat C-terminal domain	5.6e-12	53.2	1	369-421
1582	ig	Immunoglobulin domain	1.9e-05	31.5	1	438-499
1582	LRRNT	Leucine rich repeat N-terminal domain	0.0099	22.5	1	28-68
1583	Nucleoplasmin	Nucleoplasmin	4.4	-94.1	1	131-199
1587	IBR	IBR domain	1.3e-13	58.7	1	237-298
1587	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0053	20.0	1	168-213
1591	TPR	TPR Domain	4.1e-13	57.0	3	254-287:288-321:322-355
1592	PHD	PHD-finger	0.042	2.9	2	684-725:1117-1163
1592	DNA_ligase_ZBD	NAD-dependent DNA ligase C4 zinc finger	5.2	0.3	1	904-927
1593	Collagen	Collagen triple helix repeat (20 copies)	5.9	-64.0	1	302-360
1593	LIM	LIM domain	5.9	-18.2	1	841-870
1595	Peptidase_M1	Peptidase family M1	6.4e-44	159.3	1	7-279
1600	thyroglobulin_1	Thyroglobulin type-1 repeat	3.1e-06	34.1	1	38-118
1604	ig	Immunoglobulin domain	7	8.2	1	34-92
1605	PHD	PHD-finger	0.59	-7.8	1	585-644
1606	zf-CXXC	CXXC zinc finger	1.7e-21	84.9	1	50-96
1606	F-box	F-box domain	5e-06	33.4	2	545-602:713-762
1606	PHD	PHD-finger	0.062	1.3	1	207-271
1606	rubredoxin	Rubredoxin	3.6	-9.0	1	229-276
1611	L27	L27 domain	3.5	5.2	1	285-341
1612	fn3	Fibronectin type III domain	0.68	5.6	1	357-443
1613	rrm	RNA recognition motif.	3.8e-14	60.4	1	151-221
1614	SRCR	Scavenger receptor cysteine-rich domain	2.2e-26	101.1	1	52-145
1616	ldl_recept_a	Low-density lipoprotein receptor domain	0.12	8.2	1	68-114
1616	Tropomyosin	Tropomyosin	7.3	-118.6	1	216-441
1617	B56	Protein phosphatase 2A regulatory B subunit	3.3	-315.0	1	146-232

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1618	S1	S1 RNA binding domain	6.7e-10	46.3	1	352-429
1618	HHH	Helix-hairpin-helix motif	3.8	12.3	1	173-202
1619	trypsin	Trypsin	5.9e-09	43.2	1	30-190
1623	FlgI	Flagellar P-ring protein	6.7e-19	76.2	1	46-257
1623	FlgH	Flagellar L-ring protein	1.5	-75.1	1	1-73
1624	Dihydroorotase	Dihydroorotase-like	9.9	-195.7	1	1-187
1625	Semialdehyde_dhC	Semialdehyde dehydrogenase, dimerisat	1.3e-54	194.8	1	137-338
1625	Semialdehyde_dh	Semialdehyde dehydrogenase, NAD bindi	2.3e-23	91.1	1	7-128
1626	FDX-ACB	Ferredoxin-fold anticodon binding domain	1e-43	158.6	1	83-176
1628	HTH_1	Bacterial regulatory helix-turn-helix	1.5e-13	58.4	1	7-66
1628	LysR_substrate	LysR substrate binding domain	2.5e-08	41.1	1	90-281
1628	Hpt	Hpt domain	7.8	-35.7	1	65-156
1631	PEP-utilizers_C	PEP-utilizing enzyme, TIM barrel doma	1.5e-10	-43.4	1	58-174
1632	OTCace	Aspartate/ornithine carbamoyltransferase, A	0.24	-67.2	1	432-546
1632	Replicase	Replicase family	2.9	-102.2	1	399-576
1634	ribonuclease_T2	Ribonuclease T2 family	0.00089	-47.2	1	31-165
1638	efhand	EF hand	5.9e-10	46.5	4	38-66:74-102:111-139:147-175
1639	PCI	PCI domain	0.013	19.5	1	165-246
1641	Cys_knot	Cystine-knot domain	0.011	-2.5	1	227-337
1641	DAN	DAN domain	0.28	-29.8	1	199-327
1643	Ribosomal_L23	Ribosomal protein L23	9.6e-13	55.8	1	197-276
1645	tsp_1	Thrombospondin type 1 domain	0.0026	21.0	5	420-476:480-534:541-601:607-663:669-718
1647	Arginosuc_synth	Arginosuccinate synthase	1.3e-07	-97.2	1	45-196
1651	vwa	von Willebrand factor type A domain	1.1e-33	125.4	1	89-326
1652	ig	Immunoglobulin domain	2.4e-09	44.5	2	34-117:220-296
1658	thioredo	Thioredoxin	6.9e-104	358.5	2	324-432:459-570
1658	glutaredoxin	Glutaredoxin	7.4	-4.2	1	482-544
1662	Hist deacetyl	Histone deacetylase family	5.9e-61	215.9	1	857-1434
1666	wap	WAP-type (Whey Acidic Protein) 'four-disulfi	7.4e-15	62.8	1	72-116
1667	KRAB	KRAB box	1e-26	102.2	1	106-146
1672	ig	Immunoglobulin domain	3.5e-11	50.6	3	146-203:245-295:331-405
1674	Transposase_22	L1 transposable element	1.5e-51	184.7	1	6-281
1676	Ribosomal_S2	Ribosomal protein S2	0.19	-72.3	1	48-145
1677	Patatin	Patatin-like phospholipase	1.4e-36	135.0	1	132-301
1678	ig	Immunoglobulin domain	7.6	7.9	1	35-126
1678	Gemini_mov	Geminivirus putative	9.4	-42.6	1	51-131

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
		movement protein				
1684	adh_short	short chain dehydrogenase	1.3e-32	121.8	1	2-244
1685	UPAR_LY6	u-PAR/Ly-6 domain	0.0039	12.2	1	131-213
1686	pkinase	Protein kinase domain	2e-43	157.7	1	553-900
1686	Huntingtin	Huntingtin	7.3	-163.8	1	520-893
1687	HRM	Hormone receptor domain	7.8e-05	29.5	1	82-134
1688	SH3	SH3 domain	5.4e-22	86.5	1	150-206
1690	ACAT	Sterol O-acyltransferase	6	-109.5	1	181-304
1693	LRR	Leucine Rich Repeat	4.3e-34	126.7	10	505-528:529-554:555-573:575-598:613-632:634-657:659-684:686-708:709-732:738-763
1694	SH3	SH3 domain	0.00089	19.6	1	19-73
1697	Metallothio_11	Metallothionein family 11	5.8	-11.1	1	36-81
1701	cystatin	Cystatin domain	0.01	11.8	1	32-125
1704	TPR	TPR Domain	9	6.5	1	122-155
1705	Ribosomal_S26e	Ribosomal protein S26e	2.1e-16	68.0	1	133-231
1706	ank	Ankyrin repeat	5.5e-30	113.1	3	381-413:414-446:450-482
1706	TPR	TPR Domain	1.6e-06	35.1	4	3-36:43-76:164-197:205-238
1706	LRR	Leucine Rich Repeat	0.0014	25.4	4	716-743:744-764:775-802:835-859
1706	Tropomodulin	Tropomodulin	2.6	-158.7	1	248-839
1708	zf-C2H2	Zinc finger, C2H2 type	3.6e-23	90.4	4	51-74:205-227:233-255:261-284
1708	zf-BED	BED zinc finger	7.7	-6.3	1	246-285
1709	Pep_M12B_propep	Reprolysins family propeptide	0.055	-20.1	1	120-202
1710	TIG	IPT/TIG domain	1.3e-100	347.7	10	620-705:708-788:793-876:883-988:1084-1169:1174-1254:1257-1336:1341-1423:1424-1511:1516-1602
1711	pp-binding	Phosphopantetheine attachment site	0.048	12.0	1	201-255
1711	HK	Hydroxyethylthiazole kinase family	2.9	-161.9	1	12-232
1711	ketoacyl-synt	Beta-ketoacyl synthase, N-terminal domain	4	-114.1	1	265-397
1712	IGFBP	Insulin-like growth factor binding protein	8.8e-26	99.1	1	40-99
1712	thyroglobulin_1	Thyroglobulin type-1 repeat	4.6e-05	29.5	1	264-323
1714	Paralemmmin	Paralemmmin	4.2e-26	100.1	1	101-439

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1715	rvt	Reverse transcriptase	3.1e-08	40.8	1	2-147
1717	A2M_N	Alpha-2-macroglobulin family N-terminal r	0	1082.3	1	52-684
1717	A2M	Alpha-2-macroglobulin family	0	1184.5	1	776-1530
1717	TCTP	Translationally controlled tumor protein	0.0013	-47.0	1	1172-1249
1717	prenyltrans	Prenyltransferase and squalene oxidase re	7.6	3.0	1	1296-1332
1717	TSPN	Thrombospondin N-terminal -like domain	8.2	-57.8	1	34-202
1718	cadherin	Cadherin domain	9.7e-29	108.9	3	68-159:341-425:439-543
1721	MBOAT	MBOAT family	0.38	-121.1	1	3-173
1722	p450	Cytochrome P450	9.4e-48	172.1	1	86-527
1723	DUF270	Protein of unknown function, DUF270	0.12	-272.7	1	9-284
1725	ig	Immunoglobulin domain	0.75	16.2	1	34-116
1729	PA	PA domain	1.4e-29	111.7	1	521-626
1729	Glyco_hydro_47	Glycosyl hydrolase family 47	6.2e-13	28.4	1	99-364
1731	7tm_1	7 transmembrane receptor (rhodopsin family)	3.1e-62	220.2	1	50-293
1731	7tm_5	7TM chemoreceptor	1.7	-157.3	1	31-289
1731	7tm_3	7 transmembrane receptor	6.1	-155.5	1	39-302
1732	ig	Immunoglobulin domain	9.3e-16	65.8	2	49-125:169-240
1732	Adeno_E3_CR1	Adenovirus E3 region protein CR1	8.5	-24.2	1	171-251
1734	p450	Cytochrome P450	0.0069	-119.1	1	51-492
1735	profilin	Profilin	5.1e-06	33.3	1	955-1071
1735	Transposase_22	L1 transposable element	0.00026	-102.7	1	731-1016
1735	KE2	KE2 family protein	7.8	-47.5	1	765-838
1739	IL3	Interleukin-3	8.7	-38.1	1	121-224
1742	PAS	PAS domain	0.024	21.2	1	348-413
1743	transmembrane4	Tetraspanin family	0.87	-77.9	1	5-194
1744	Dynein_heavy	Dynein heavy chain	2e-253	855.3	1	4-781
1745	SCP	SCP-like extracellular protein	9.8e-36	132.1	1	4-180
1745	granulin	Granulin	0.32	-8.1	1	173-206
1749	sugar_tr	Sugar (and other) transporter	0.26	-152.9	1	260-692
1749	oxidored_q1	NADH-Ubiquinone/plastoquinone	1.6	-155.3	1	391-674
1749	FecCD	FecCD transport family	4.7	-214.9	1	473-686
1749	Herpes_HEPA	Herpesvirus DNA helicase/primase compl	5.4	-457.3	1	77-605
1749	PsbT	Photosystem II reaction centre T prote	5.9	5.1	1	545-572
1749	Bac_rhodopsin	Bacteriorhodopsin	6.8	-137.3	1	295-496
1749	C4dic_mal_transporter	C4-dicarboxylate transporter/malic aci	9.9	-183.4	1	265-477

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SEQ ID	Model	Description	E-value	Score	Repeats	Position
1750	ATP-synt_A	ATP synthase A chain	8.1	-80.8	1	837-958
1751	SDF	Sodium:dicarboxylate symporter family	2.7	-254.2	1	275-426
1753	ig	Immunoglobulin domain	9.9e-19	75.7	5	49-124:162-219:261-310:345-400:432-496
1753	fn3	Fibronectin type III domain	0.00052	26.8	1	514-606
1755	sugar_tr	Sugar (and other) transporter	0.13	-144.2	1	1-366
1755	PUCC	PUCC protein	2.3	-267.4	1	21-314
1755	Nuc_H_symport	Nucleoside H ⁺ symporter	4.4	-267.2	1	1-356
1755	7tm_5	7TM chemoreceptor	4.8	-165.5	1	59-281
1755	Competence	Competence protein	5.1	-101.6	1	16-209
1755	Ammonium_transp	Ammonium Transporter Family	5.4	-242.0	1	67-380
1755	BenE	Benzoate membrane transport protein	8.1	-335.2	1	69-351
1757	Exo_endo_phos	Endonuclease/Exonuclease/phosphatase fa	1.3e-20	81.9	1	367-788
1758	K_tetra	K ⁺ channel tetramerisation domain	2.9	-38.6	1	114-214
1759	HK	Hydroxyethylthiazole kinase family	3	-162.1	1	303-502
1760	Peptidase_C20	Type IV leader peptidase family	6.6	-187.3	1	29-187
1762	SSF	Sodium:solute symporter family	4.2e-256	864.2	1	39-477
1762	MVIN	Virulence factor MVIN	7.1	-250.2	1	68-548
1762	PNTB	NAD(P) transhydrogenase beta subunit	8.1	-394.0	1	11-300
1762	7tm_5	7TM chemoreceptor	9.1	-170.5	1	75-352
1762	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	9.1	-170.9	1	145-463
1763	LRR	Leucine Rich Repeat	2e-37	137.7	11	61-84:85-108:109-132:133-156:157-180:181-204:205-228:253-276:277-300:301-324:349-371
1763	LRRCT	Leucine rich repeat C-terminal domain	1.9e-07	38.2	1	358-411
1763	ig	Immunoglobulin domain	8.5e-05	29.4	1	428-486
1763	LRRNT	Leucine rich repeat N-terminal domain	0.00023	27.9	1	30-59
1764	Reprolysin	Reprolysin (M12B) family zinc metalloprote	1e-21	85.6	1	156-359
1764	tsp_1	Thrombospondin type 1 domain	2.5e-06	34.5	1	422-491
1769	C2	C2 domain	2.5e-66	233.8	2	249-337:383-471
1771	cadherin	Cadherin domain	2.7e-79	276.8	5	140-235:249-343:359-451:465-556:607-697
1774	transmembran	Tetraspanin family	6.4e-59	209.2	1	458-702

Table 4B
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SEQ ID	Model	Description	E-value	Score	Repeats	Position
	e4					
1775	7tm_1	7 transmembrane receptor (rhodopsin family)	7.9e-05	-5.9	1	34-333
1775	Srg	C.elegans Srg family integral membrane prote	9.3	-223.5	1	111-306
1778	synaptobrevin	Synaptobrevin	4.1e-32	120.1	1	110-198
1779	trefoil	Trefoil (P-type) domain	3.9	-11.1	1	229-254
1780	MHC_I	Class I Histocompatibility antigen, domains	2.6e-89	310.1	1	25-199
1780	ig	Immunoglobulin domain	3.3e-06	34.0	1	194-259
1782	ABC_tran	ABC transporter	2.4e-19	77.7	1	448-626
1783	SNF	Sodium:neurotransmitter symporter famil	0	1189.5	1	203-747
1783	Herpes_glycop	Herpesvirus glycoprotein M	7.2	-262.5	1	460-801
1783	UPF0118	Domain of unknown function DUF20	8	-131.6	1	240-582
1783	Cyto_ox_2	Cytochrome oxidase subunit II	9	-243.9	1	467-696
1819	Y_phosphatase	Protein-tyrosine phosphatase	1.2e-103	357.8	1	1277-1494
1819	fn3	Fibronectin type III domain	1.2e-51	185.1	7	461-541:552-634:641-719:730-812:819-900:908-990:998-1087
1821	7tm_1	7 transmembrane receptor (rhodopsin family)	4.4	-116.1	1	206-413
1822	Metallophos	Calcineurin-like phosphoesterase	1.5	2.4	1	66-252

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Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
913	1ae7		472	598	5.1e-25	0.14	-0.09		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE PLA2, PHOSPHATIDE SN-2 ACYLHYDROLASE; HYDROLASE, PHOSPHOLIPASE A2, LIPID DEGRADATION, PRESYNAPTIC 2 NEUROTOXIN, VENOM
913	1aut	L	468	569	8.5e-19	0.17	0.03		ACTIVATED PROTEIN C; CHAIN: C, L, D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
913	1aut	L	553	637	3.4e-15	0.01	-0.13		ACTIVATED PROTEIN C; CHAIN: C, L, D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
913	1aut	L	784	842	5.1e-16	0.04	0.54		ACTIVATED PROTEIN C; CHAIN: C, L, D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
913	1bk9		470	597	3.4e-26	0.32	-0.18		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE HYDROLASE, PHOSPHOLIPASE A2, PLATELET AGGREGATION INHIBITOR, 2 PBPB HEADER MODRES
913	1bk9		510	637	1.4e-25	0.17	-0.15		PHOSPHOLIPASE A2;	HYDROLASE HYDROLASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: NULL;	PHOSPHOLIPASE A2, PLATELET AGGREGATION INHIBITOR, 2 PBPB HEADER MODRES
913	1dan	L	430	520	7e-11	-0.24	0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
913	1dan	L	455	565	8.5e-21	-0.06	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
913	1dan	L	482	602	3.4e-26	0.06	0.34		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
913	1dan	L	527	637	6.8e-21	-0.23	0.60		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
913	1dan	L	782	897	3.4e-19	-0.10	0.07		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
913	1dqb	A	468	558	3.4e-21	0.28	0.15		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
913	1dqb	A	796	876	1.4e-17	0.03	-0.09		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
913	1dva	L	430	520	7e-11	0.08	0.39		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
913	1dva	L	468	565	3.4e-19	0.05	0.25		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
913	1dva	L	507	602	3.4e-19	0.12	0.53		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
913	1dva	L	551	637	1.7e-16	0.18	0.81		VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	
									DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
913	1dva	L	784	852	5.1e-14	-0.17	0.05		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
									DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
913	1dva	L	795	897	3.4e-17	-0.13	0.07		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
									DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
913	1dx5	I	395	508	1.4e-15	-0.16	0.11		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
913	1dx5	I	454	553	1.4e-17	0.24	0.18		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
913	1dx5	I	470	593	6.8e-29	0.29	0.86		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
913	1dx5	I	721	836	2.8e-14	-0.08	0.10		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
913	1dx5	I	784	886	8.5e-18	-0.12	0.07		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
913	1emn		430	509	2.8e-15	0.40	0.86		CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H; FIBRILLIN; CHAIN: NULL;	PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
913	1emn		552	611	3.4e-21	-0.45	0.74		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
913	1emn		683	752	5.6e-10	0.02	-0.05		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
913	1emn		795	857	1e-19	-0.23	0.83		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL ID score	Compound	PDB annotation
913	1emn		838	908	1.1e-09	-0.55	0.12		FIBRILLIN; CHAIN: NULL;	FRAGMENT, MATRIX PROTEIN
										MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
913	1ext	A	453	624	3.4e-31	0.14	0.36		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
913	1ext	A	70	220	1.3e-08	0.25	-0.19		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
913	1ext	A	785	888	8.5e-21	0.34	-0.11		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
913	1fak	L	430	520	7e-11	0.04	0.21		BLOOD COAGULATION FACTOR VIIA; CHAIN: L;	BLOOD CLOTTING COMPLEX(SERINE
									BLOOD COAGULATION FACTOR VIIA; CHAIN: H;	PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE
									SOLUBLE TISSUE FACTOR; CHAIN: T;	PROTEASE, COMPLEX, CO-
									5L15; CHAIN: I;	FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX
913	1fak	L	468	565	6.8e-20	0.27	0.39		BLOOD COAGULATION FACTOR VIIA; CHAIN: L;	BLOOD CLOTTING COMPLEX(SERINE
									BLOOD COAGULATION FACTOR VIIA; CHAIN: H;	PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE
									SOLUBLE TISSUE FACTOR; CHAIN: T;	PROTEASE, COMPLEX, CO-
									5L15; CHAIN: I;	FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
913	1fak	L	506	602	1.7e-20	0.18	0.29		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	(SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
913	1fak	L	552	637	8.5e-16	-0.15	0.19		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
913	1fak	L	795	897	6.8e-17	-0.07	0.30		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
913	1h4u	A	227	446	3.4e-55	0.49	0.95	-	NIDOGEN-I; CHAIN: A;	EXTRACELLULAR MATRIX PROTEIN EXTRACELLULAR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
913	1hj7	A	114	187	2.8e-09	0.32	-0.20		LDL RECEPTOR; CHAIN: A;	MATRIX PROTEIN
										CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
913	1hj7	A	595	720	1.4e-12	-0.65	0.10		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
										CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
913	1hj7	A	784	837	1.4e-18	0.66	1.00		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
										CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
913	1hj7	A	800	882	1.7e-21	0.19	0.70		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
										CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
913	1hj7	A	840	928	1.4e-08	-0.22	0.00		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
										CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
913	1igr	A	96	253	1.3e-08	0.05	-0.19		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
										LIPID TRANSPORT LDL RECEPTOR; BETA-PROPELLER
913	1ijq	A	344	508	6.8e-15	0.23	0.06		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A, B;	GLYCOPROTEIN GLYCOPROTEIN
										GLYCOPROTEIN GLYCOPROTEIN
913	1kdo		129	286	1.1e-09	0.24	-0.20		LAMININ; CHAIN: NULL;	
913	1kdo		172	325	1.3e-08	0.02	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
913	1kdo		419	554	9.8e-11	0.11	-0.15		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
913	1kdo		474	633	1.7e-21	0.31	-0.07		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
913	1kdo		70	231	1.4e-11	0.16	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
913	1pfx	L	454	578	1.7e-18	0.10	-0.03		FACTOR IXA; CHAIN: C ₁ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
913	1pfx	L	478	610	8.5e-21	0.02	0.11		FACTOR IXA; CHAIN: C ₁ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
913	1pfx	L	522	637	3.4e-19	0.07	-0.03		FACTOR IXA; CHAIN: C ₁ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
913	1pfx	L	787	888	5.1e-17	-0.06	0.00		FACTOR IXA; CHAIN: C ₁ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
913	1qfk	L	784	859	1.7e-15	0.18	0.10		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
913	1vap	A	472	597	3.4e-24	0.14	-0.14		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
913	1vap	A	511	637	1.7e-23	0.19	-0.17		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
913	1vmo	A	121	235	3.4e-12	0.70	-0.08		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I I VMO 3	
913	1xka	L	558	637	5.1e-14	0.27	0.81		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
913	1xka	L	784	842	3.4e-14	0.11	0.68		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
913	9wga	A	102	272	1.3e-14	0.07	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
913	9wga	A	353	493	4.2e-10	0.34	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
914	1dpt	A	2	111	1.1e-33			130.55	(ISOLECTIN 2) 9WGA 3 D-DOPACHROME TAUTOMERASE; CHAIN: A, B, C;	CYTOKINE CYTOKINE, GROWTH FACTOR, TAUTOMERASE
914	1dpt	A	2	115	2.8e-33			133.05	D-DOPACHROME TAUTOMERASE; CHAIN: A, B, C;	CYTOKINE CYTOKINE, GROWTH FACTOR, TAUTOMERASE
914	1dpt	A	2	95	2.8e-33	0.98	1.00		D-DOPACHROME TAUTOMERASE; CHAIN: A, B, C;	CYTOKINE CYTOKINE, GROWTH FACTOR, TAUTOMERASE
914	1f1m		2	109	9.8e-37			60.34	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: NULL;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
914	1f1m		2	95	1.4e-36	0.69	1.00		MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: NULL;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
914	1gd0	A	2	111	5.6e-37			60.28	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	IMMUNE SYSTEM MIF, MIF, MACROPHAGE MIGRATION INHIBITORY FACTOR,
914	1gd0	A	2	123	1.1e-36			69.95	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	IMMUNE SYSTEM MIF, MIF, MACROPHAGE MIGRATION INHIBITORY FACTOR,
914	1gd0	A	2	95	1.1e-36	0.69	1.00		MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	IMMUNE SYSTEM MIF, MIF, MACROPHAGE MIGRATION INHIBITORY FACTOR,
914	1mfi	A	2	120	4.2e-37			67.20	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	CYTOKINE PHENYLPIRUVATE TAUTOMERASE; CYTOKINE, MACROPHAGE, INFLAMMATORY RESPONSE, TAUTOMERASE

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
914	1mfi	A	2	95	4.2e-37	0.85	1.00		MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	CYTOKINE PHENYLPIRUVATE TAUTOMERASE; CYTOKINE, MACROPHAGE, INFLAMMATORY RESPONSE, TAUTOMERASE
915	1dpt	A	2	131	2.8e-42	0.69	1.00		D-DOPACHROME TAUTOMERASE; CHAIN: A, B, C;	CYTOKINE CYTOKINE, GROWTH FACTOR, TAUTOMERASE
915	1dpt	A	2	131	2.8e-42			163.64	D-DOPACHROME TAUTOMERASE; CHAIN: A, B, C;	CYTOKINE CYTOKINE, GROWTH FACTOR, TAUTOMERASE
915	1gd0	A	2	127	1.4e-44	0.60	1.00		MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	IMMUNE SYSTEM MIF; MIF, MACROPHAGE MIGRATION INHIBITORY FACTOR,
915	1gd0	A	2	130	1.4e-44			63.03	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	IMMUNE SYSTEM MIF; MIF, MACROPHAGE MIGRATION INHIBITORY FACTOR,
915	1mfi	A	2	127	9.8e-46	0.72	0.98		MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	CYTOKINE PHENYLPIRUVATE TAUTOMERASE; CYTOKINE, MACROPHAGE, INFLAMMATORY RESPONSE, TAUTOMERASE
916	1a0h	A	284	467	1.7e-29	-0.30	0.39		MEIZOTHROMBIN; CHAIN: A, B, D, E; D-PHE-PRO-ARG; CHAIN: C, F;	PROTEASE (SERINE PROTEASE/INHIBITOR) DESFI; PPAC; SERINE PROTEASE, COAGULATION, THROMBIN, PROTHROMBIN, 2
916	1a0j	A	11	248	4.2e-96			190.46	TRYPSIN; CHAIN: A, B, C, D;	MEIZOTHROMBIN, COMPLEX (SERINE PROTEASE/INHIBITOR)
916	1a0j	A	445	682	2.8e-96	0.93	1.00		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
916	1a0j	A	445	682	2.8e-96	0.93	1.00		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PME score	SEQFOI D score	Compound	PDB annotation
916	1a0j	A	445	682	2.8e-96			193.09	TRYPSIN; CHAIN: A, B, C, D;	HYDROLASE SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
916	1a5i	A	1	247	5.6e-83			214.60	PLASMINOGEN ACTIVATOR; CHAIN: A; GLU-GLY-ARG CHLOROMETHYL KETONE; CHAIN: I;	COMPLEX (SERINE PROTEASE/INHIBITOR) (DELTAPEK)DSPALPHA1; EGRCMK; SERINE PROTEASE, FIBRINOLYTIC ENZYMES, PLASMINOGEN 2 ACTIVATORS
916	1a5i	A	430	681	1.2e-85			219.75	PLASMINOGEN ACTIVATOR; CHAIN: A; GLU-GLY-ARG CHLOROMETHYL KETONE; CHAIN: I;	COMPLEX (SERINE PROTEASE/INHIBITOR) (DELTAPEK)DSPALPHA1; EGRCMK; SERINE PROTEASE, FIBRINOLYTIC ENZYMES, PLASMINOGEN 2 ACTIVATORS
916	1aut	C	11	246	1.4e-78			182.91	ACTIVATED PROTEIN C; CHAIN: C, I; D-PHE-PRO- MAL; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
916	1aut	C	445	680	5.1e-79			185.86	ACTIVATED PROTEIN C; CHAIN: C, I; D-PHE-PRO- MAL; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
916	1aut	L	159	252	8.4e-15	0.32	-0.03		ACTIVATED PROTEIN C; CHAIN: C, I; D-PHE-PRO- MAL; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
916	1b2i	A	284	367	1.4e-28	-0.06	1.00		PLASMINOGEN; CHAIN: A;	HYDROLASE SERINE PROTEASE, FIBRINOLYSIS, LYSINE-BINDING DOMAIN, 2 PLASMINOGEN, KRINGLE 2, HYDROLASE
916	1b2i	A	76	153	4.2e-21	0.20	-0.14		PLASMINOGEN; CHAIN: A;	HYDROLASE SERINE PROTEASE, FIBRINOLYSIS, LYSINE-BINDING DOMAIN, 2 PLASMINOGEN, KRINGLE 2, HYDROLASE
916	1b2i	A	7	93	2.8e-28			70.19	PLASMINOGEN; CHAIN: A;	HYDROLASE SERINE PROTEASE, FIBRINOLYSIS, LYSINE-BINDING DOMAIN, 2 PLASMINOGEN, KRINGLE 2, HYDROLASE
916	1bf9		162	201	1.2e-13	0.80	1.00		FACTOR VII; CHAIN: NULL;	BLOOD COAGULATION BLOOD COAGULATION, EGF, HYDROLASE, SERINE PROTEASE
916	1brt	P	11	248	4.2e-87			180.84	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
916	1brt	P	445	682	1.4e-88	0.96	1.00		ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
916	1brt	P	445	682	1.4e-88			183.63	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
916	1c5y	B	11	248	2.8e-85			214.59	UROKINASE-TYPE PLASMINOGEN ACTIVATOR; CHAIN: A;	BLOOD CLOTTING SELECTIVE, SI SITE INHIBITOR, STRUCTURE- BASED DRUG DESIGN, 2 UROKINASE, TRYPSIN, THROMBIN
916	1c5y	B	445	682	8.5e-86			217.96	UROKINASE-TYPE PLASMINOGEN	BLOOD CLOTTING SELECTIVE, SI SITE INHIBITOR, STRUCTURE-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/ROL D score	Compound	PDB annotation
									ACTIVATOR; CHAIN: A; UROKINASE-TYPE PLASMINOGEN ACTIVATOR; CHAIN: B; PLASMINOGEN; ICEA 7 CHAIN: A, B, ICEA 8	BASED DRUG DESIGN, 2 UROKINASE, TRYPSIN, THROMBIN SERINE PROTEASE K1PG; ICEA 10
916	1cea	A	10	92	1.4e-26			65.46	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE
916	1cxw	A	102	151	3.4e-20	0.72	1.00		HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE
916	1cxw	A	37	95	7e-24			60.11	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE
916	1dan	H	11	251	1.1e-77			170.95	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D- PHE-PHE-ARG- CHLOROMETHYLKETO NE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO- FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
916	1dan	L	133	251	3.4e-18	0.16	-0.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D- PHE-PHE-ARG- CHLOROMETHYLKETO NE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO- FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
916	1dan	L	162	250	1.4e-27	0.23	0.68		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D- PHE-PHE-ARG- CHLOROMETHYLKETO NE (DFFRCMK) WITH	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO- FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
916	1ddj	A	1	248	2.8e-89			176.67	CHAIN: C; PLASMINOGEN; CHAIN: A, B, C, D;	BLOOD CLOTTING PLASMINOGEN, CATALYTIC DOMAIN
916	1ddj	A	428	682	7e-95	0.87	1.00		PLASMINOGEN; CHAIN: A, B, C, D;	BLOOD CLOTTING PLASMINOGEN, CATALYTIC DOMAIN
916	1ddj	A	429	682	7e-95			187.88	PLASMINOGEN; CHAIN: A, B, C, D;	BLOOD CLOTTING PLASMINOGEN, CATALYTIC DOMAIN
916	1dlk	B	11	248	4.2e-82			179.88	DELTA- CHYMOTRYPSIN; CHAIN: A, C; DELTA- CHYMOTRYPSIN; CHAIN: B, D;	HYDROLASE DELTA- CHYMOTRYPSIN, PEPTIDIC INHIBITOR, CHLOROMETHYL KETONE
916	1dlk	B	445	682	1.3e-83			183.37	DELTA- CHYMOTRYPSIN; CHAIN: A, C; DELTA- CHYMOTRYPSIN; CHAIN: B, D;	HYDROLASE DELTA- CHYMOTRYPSIN, PEPTIDIC INHIBITOR, CHLOROMETHYL KETONE
916	1dva	L	162	250	1.4e-27	0.39	0.47		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
916	1dva	L	4	106	4.2e-19			64.99	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
916	1dx5	I	5	126	2.8e-18			54.24	PEPTIDE E-76; CHAIN: X, Y;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
916	1e88	A	1	125	5.6e-34			56.65	FIBRONECTIN; CHAIN: A;	EXTRACELLULAR MATRIX GLYCOPROTEIN EXTRACELLULAR MATRIX GLYCOPROTEIN
916	1e88	A	97	207	6.8e-21	0.55	0.33		FIBRONECTIN; CHAIN: A;	EXTRACELLULAR MATRIX GLYCOPROTEIN EXTRACELLULAR MATRIX GLYCOPROTEIN
916	1ekb	B	11	246	9.8e-83			190.18	ENTEROPEPTIDASE; CHAIN: A; ENTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-LYS-PEPTIDE; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR ENTEROKINASE, HEAVY CHAIN; ENTEROKINASE, LIGHT CHAIN; ENTEROPEPTIDASE, TRYPSINOGEN ACTIVATION, 2 HYDROLASE/HYDROLASE INHIBITOR
916	1ekb	B	445	680	1.4e-82			193.02	ENTEROPEPTIDASE; CHAIN: A; ENTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-LYS-PEPTIDE; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR ENTEROKINASE, HEAVY CHAIN; ENTEROKINASE, LIGHT CHAIN; ENTEROPEPTIDASE, TRYPSINOGEN ACTIVATION, 2 HYDROLASE/HYDROLASE INHIBITOR

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
916	1elt		11	245	2.8e-81			175.26	ELASTASE; 1ELT 4 CHAIN: NULL; 1ELT 5	SERINE PROTEINASE
916	1elt		445	679	2.8e-81			178.10	ELASTASE; 1ELT 4 CHAIN: NULL; 1ELT 5	SERINE PROTEINASE
916	1ext	A	146	273	5.1e-13	0.33	-0.13		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
916	1f7z	A	11	248	8.4e-92			170.59	TRYPSIN II, ANIONIC; CHAIN: A; PANCREATIC TRYPSIN INHIBITOR; CHAIN: I;	HYDROLASE/HYDROLASE INHIBITOR BPTI SERINE PROTEASE, TRYPSIN PRECURSOR
916	1f7z	A	445	682	2.8e-92	0.92	1.00		TRYPSIN II, ANIONIC; CHAIN: A; PANCREATIC TRYPSIN INHIBITOR; CHAIN: I;	HYDROLASE/HYDROLASE INHIBITOR BPTI SERINE PROTEASE, TRYPSIN PRECURSOR
916	1fak	L	162	250	1.4e-27	0.35	0.66		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO- FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
916	1fak	L	4	106	4.2e-19			59.97	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO- FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
916	1ftw	A	11	249	2.8e-81			169.75	BETA-ACROSIN HEAVY CHAIN; CHAIN: A; BETA-ACROSIN LIGHT CHAIN; CHAIN: L	HYDROLASE ANTI-PARALLEL BETA-BARREL
916	1ftw	A	445	689	4.2e-81			177.29	BETA-ACROSIN HEAVY CHAIN; CHAIN: A; BETA-ACROSIN LIGHT CHAIN; CHAIN: L	HYDROLASE ANTI-PARALLEL BETA-BARREL
916	1ftz	A	11	249	2.8e-81			171.91	BETA-ACROSIN HEAVY CHAIN; CHAIN: A; BETA-ACROSIN LIGHT CHAIN; CHAIN: L	HYDROLASE ANTI-PARALLEL BETA-BARREL
916	1ftz	A	445	689	5.6e-82			177.71	BETA-ACROSIN HEAVY CHAIN; CHAIN: A; BETA-ACROSIN LIGHT CHAIN; CHAIN: L	HYDROLASE ANTI-PARALLEL BETA-BARREL
916	1fhi	A	11	248	2.8e-97			186.43	TRYPSIN; CHAIN: A;	HYDROLASE SERINE PROTEASE, HYDROLASE
916	1fhi	A	445	682	5.6e-98	1.03	1.00		TRYPSIN; CHAIN: A;	HYDROLASE SERINE PROTEASE, HYDROLASE
916	1fhi	A	445	682	5.6e-98			189.59	TRYPSIN; CHAIN: A;	HYDROLASE SERINE PROTEASE, HYDROLASE
916	1fxy	A	11	249	4.2e-86			178.61	COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: L	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
916	1fxy	A	445	682	5.6e-87	1.02	1.00		COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/ROL D score	Compound	PDB annotation
916	1fxy	A	445	683	5.6e-87			181.30	NE (PPACK) WITH CHAIN: 1;	COMPLEX (PROTEASE/INHIBITOR)
									COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: 1;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACX, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
916	1gct	A	1	248	4.2e-80			174.02	HYDROLASE (SERINE PROTEINASE) GAMMA-CHYMOTRYPSIN *A (E.C.3.4.21.1) (SP*H 7.0) IGCT 3	
916	1gct	A	431	682	2.8e-83			176.84	HYDROLASE (SERINE PROTEINASE) GAMMA-CHYMOTRYPSIN *A (E.C.3.4.21.1) (SP*H 7.0) IGCT 3	
916	1hq8	A	49	163	2.8e-29			82.88	NKG2-D; CHAIN: A;	APOPTOSIS HOMODIMER, CIS-PROLINE
916	1i5k	A	10	92	1.4e-28			68.60	PLASMINOGEN; CHAIN: A, B; M PROTEIN; CHAIN: C, D;	BLOOD CLOTTING HUMAN PLASMINOGEN KRINGLE-2, KRINGLES, VEK-30
916	1i5k	A	78	153	8.4e-22	0.12	-0.18		PLASMINOGEN; CHAIN: A, B; M PROTEIN; CHAIN: C, D;	BLOOD CLOTTING HUMAN PLASMINOGEN KRINGLE-2, KRINGLES, VEK-30
916	1i71	A	10	96	2.8e-30			73.08	APOLIPROTEIN(A); CHAIN: A;	HYDROLASE APO(A); ALIPOPTEIN(A), KRINGLE, PROTEIN-LIGAND INTERACTION, 2 LYSINE BINDING, CRYSTAL STRUCTURE
916	1i71	A	77	154	8.4e-21	0.26	-0.13		APOLIPROTEIN(A); CHAIN: A;	HYDROLASE APO(A); ALIPOPTEIN(A), KRINGLE,

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
916	1j7m	A	105	150	5.1e-19	0.93	1.00		MATRIX METALLOPROTEINASE 2; CHAIN: A;	PROTEIN-LIGAND INTERACTION, 2 LYSINE BINDING, CRYSTAL STRUCTURE
916	1kdu		10	94	2.8e-31			79.24	PLASMINOGEN ACTIVATION PLASMINOGEN ACTIVATOR (UROKINASE-TYPE, KRINGLE DOMAIN) IKDU 3 (U-PA K) (NMR, MINIMIZED AVERAGE STRUCTURE) IKDU 4	HYDROLASE 72 KDA TYPE IV COLLAGENASE, GELATINASE A; BETA SHEET, ALPHA HELIX
916	1kdu		285	369	7e-30	0.47	1.00		PLASMINOGEN ACTIVATION PLASMINOGEN ACTIVATOR (UROKINASE-TYPE, KRINGLE DOMAIN) IKDU 3 (U-PA K) (NMR, MINIMIZED AVERAGE STRUCTURE) IKDU 4	
916	1kdu		286	367	1.7e-32	0.43	1.00		PLASMINOGEN ACTIVATION PLASMINOGEN ACTIVATOR (UROKINASE-TYPE, KRINGLE DOMAIN) IKDU 3 (U-PA K) (NMR, MINIMIZED AVERAGE STRUCTURE) IKDU 4	
916	1klo		146	293	1e-14	0.25	-0.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
916	1kcn		10	92	2.8e-32			76.64	PLASMINOGEN; CHAIN:	SERINE PROTEASE KRINGLE,

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									NULL;	BLOOD, PLASMINOGEN, SERINE PROTEASE
916	1ktn		285	367	2.8e-28	0.21	1.00		PLASMINOGEN; CHAIN: NULL;	SERINE PROTEASE KRINGLE, BLOOD, PLASMINOGEN, SERINE PROTEASE
916	1ktn		77	153	9.8e-23	0.21	-0.09		PLASMINOGEN; CHAIN: NULL;	SERINE PROTEASE KRINGLE, BLOOD, PLASMINOGEN, SERINE PROTEASE
916	1npm	A	11	246	5.6e-80			172.80	NEUROPSIN; CHAIN: A, B;	SERINE PROTEINASE SERINE PROTEINASE, GLYCOPROTEIN
916	1npm	A	445	680	5.6e-80			175.97	NEUROPSIN; CHAIN: A, B;	SERINE PROTEINASE SERINE PROTEINASE, GLYCOPROTEIN
916	1pdc		104	148	1.2e-21	0.52	1.00		COLLAGEN-BINDING TYPE II DOMAIN SEMINAL FLUID PROTEIN PDC-109 (DOMAIN B) 1PDC.3 (NMR, BEST STRUCTURE) 1PDC.4	
916	1pdc		47	91	5.6e-18			54.17	COLLAGEN-BINDING TYPE II DOMAIN SEMINAL FLUID PROTEIN PDC-109 (DOMAIN B) 1PDC.3 (NMR, BEST STRUCTURE) 1PDC.4	
916	1pfx	C	11	248	1.1e-83			180.03	FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR, COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
916	1pfx	C	445	682	2.8e-83			181.67	FACTOR IXA; CHAIN: C; L ₁ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
916	1pfx	L	122	267	1e-18	0.17	-0.13		FACTOR IXA; CHAIN: C; L ₁ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
916	1pfx	L	162	259	4.2e-23	0.39	-0.12		FACTOR IXA; CHAIN: C; L ₁ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
916	1pml	A	286	367	8.5e-32	0.72	1.00		HYDROLASE(SERINE PROTEASE) TISSUE PLASMINOGEN ACTIVATOR KRINGLE 2 (E.C.3.4.21.68) 1PML.3	
916	1pml	A	9	94	4.2e-32			101.06	HYDROLASE(SERINE PROTEASE) TISSUE PLASMINOGEN ACTIVATOR KRINGLE 2 (E.C.3.4.21.68) 1PML.3	
916	1pml	C	286	367	1.2e-31	0.71	1.00		HYDROLASE(SERINE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PROTEASE) TISSUE PLASMINOGEN ACTIVATOR KRINGLE 2 (E.C.3.4.21.68) 1PML 3	
916	1pml	C	9	93	4.2e-32			101.45	HYDROLASE(SERINE PROTEASE) TISSUE PLASMINOGEN ACTIVATOR KRINGLE 2 (E.C.3.4.21.68) 1PML 3	
916	1pp2	L	162	284	1.7e-23	0.02	-0.18		HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2= (E.C.3.1.1.4) 1PP2 4	
916	1pyt	D	1	247	5.6e-81			182.06	PROCARBOXYPEPTIDAS E A; CHAIN: A, B; PROPROTEINASE E; CHAIN: C; CHYMOTRYPSINOGEN C; CHAIN: D;	TERNARY COMPLEX (ZYMOGEN) TC, PCPA-TG; TERNARY COMPLEX (ZYMOGEN), SERINE PROTEINASE, C-TERMINAL 2 PEPTIDASE
916	1pyt	D	431	681	8.4e-83			187.81	PROCARBOXYPEPTIDAS E A; CHAIN: A, B; PROPROTEINASE E; CHAIN: C; CHYMOTRYPSINOGEN C; CHAIN: D;	TERNARY COMPLEX (ZYMOGEN) TC, PCPA-TG; TERNARY COMPLEX (ZYMOGEN), SERINE PROTEINASE, C-TERMINAL 2 PEPTIDASE
916	1qfk	L	10	109	2.8e-18			58.07	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
916	1qfk	L	163	250	4.2e-27	0.17	0.12		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
916	1qo6	A	102	152	3.4e-21	1.10	1.00		VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C; FIBRONECTIN; CHAIN: A;	CELL ADHESION PROTEIN FIBRONECTIN MODULE PAIR, GELATIN-BINDING
916	1rfn	A	11	248	2.8e-83			181.07	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
916	1rfn	A	445	682	1.1e-82			183.25	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
916	1rtf	B	11	247	1.4e-85			229.36	TWO CHAIN TISSUE PLASMINOGEN ACTIVATOR; CHAIN: A, B;	SERINE PROTEASE (TC)-T-PA; SERINE PROTEASE, FIBRINOLYTIC ENZYMES
916	1rtf	B	445	681	1e-84			231.89	TWO CHAIN TISSUE PLASMINOGEN ACTIVATOR; CHAIN: A, B;	SERINE PROTEASE (TC)-T-PA; SERINE PROTEASE, FIBRINOLYTIC ENZYMES
916	1slw	B	11	248	2.8e-92			174.20	ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE-SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
916	1slw	B	445	682	8.4e-93	1.01	1.00		ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL

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Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
916	1slw	B	445	682	8.4e-93			176.17	ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE-SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
										COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE-SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
916	1tpg		202	285	1.4e-24	0.61	1.00		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL, 1TPG 8	PLASMINOGEN ACTIVATION
916	1tpg		45	132	9.8e-19			75.25	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL, 1TPG 8	PLASMINOGEN ACTIVATION
916	1trn	A	11	249	2.8e-94			185.24	HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR 1TRN 3 DIISOPROPYL-FLUOROPHOSPHOFLUORIDATE (DFP) 1TRN 4 HUMAN TRYPSIN, DFP INHIBITED 1TRN 6	
916	1trn	A	445	682	9.8e-95	0.85	1.00		HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR 1TRN 3 DIISOPROPYL-FLUOROPHOSPHOFLUORIDATE (DFP) 1TRN 4 HUMAN TRYPSIN, DFP INHIBITED 1TRN 6	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RIDATE (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	
916	1tm	A	445	683	9.8e-95			188.29	HYDROLASE (SERINE PROTEINASE) TRYPsin (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DISOPROPYL- FLUOROPHOSPHOFLUO RIDATE (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	
916	1urk		1	96	1.3e-34			70.09	PLASMINOGEN ACTIVATION PLASMINOGEN ACTIVATOR (UROKINASE-TYPE) (AMINO TERMINAL FRAGMENT) (NMR, 15 STRUCTURES)	
916	1urk		243	369	1.1e-46	0.46	1.00		PLASMINOGEN ACTIVATION PLASMINOGEN ACTIVATOR (UROKINASE-TYPE) (AMINO TERMINAL FRAGMENT) (NMR, 15 STRUCTURES)	
916	1xka	L	10	105	8.4e-16			50.64	BLOOD COAGULATION FACTOR XA; CHAIN: L, C ₁	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
916	2fb2		97	148	1.7e-20	0.72	1.00		FIBRONECTIN; CHAIN:	GLYCOPROTEIN GLYCOPROTEIN,

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Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
916	2hpp	P	11	92	1.4e-17			60.55	HYDROLASE(SERINE PROTEINASE) ALPHA-THROMBIN (E.C.3.4.21.5) COMPLEX WITH 2HPP 3 D-PHE-PRO-ARG-CHLOROMETHYLKETO NE (PPACK) CHLOROMETHYLKETO NE 2HPP 4 REPLACED BY A METHYLENE GROUP AND BOVINE PROTHROMBIN 2HPP 5 FRAGMENT 2 2HPP 6	FIBRONECTIN, TYPE TWO MODULE, NMR STRUCTURE, 2 GLYCOSYLATED PROTEIN, COLLAGEN
916	2hpp	P	11	92	4.2e-17			52.00	HYDROLASE(SERINE PROTEINASE) ALPHA-THROMBIN (E.C.3.4.21.5) COMPLEX WITH 2HPQ 3 D-PHE-PRO-ARG-CHLOROMETHYLKETO NE (PPACK) CHLOROMETHYLKETO NE 2HPQ 4 REPLACED BY A METHYLENE GROUP AND HUMAN PROTHROMBIN 2HPQ 5 FRAGMENT 2 2HPQ 6	
916	2pfl		148	268	1.1e-20	0.32	-0.18		HYDROLASE(SERINE PROTEINASE) PROTHROMBIN FRAGMENT 1 (RESIDUES 1 - 156) 2PFL	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
916	2pf1		1	102	2.8e-24			50.59	3 HYDROLASE/SERINE PROTEINASE) PROTHROMBIN FRAGMENT 1 (RESIDUES 1 - 156) 2PF1	
916	2pf1		265	368	1.7e-31	0.77	0.83		3 HYDROLASE/SERINE PROTEINASE) PROTHROMBIN FRAGMENT 1 (RESIDUES 1 - 156) 2PF1	
916	2pf2		148	263	8.4e-20	0.15	-0.20		3 HYDROLASE(SERINE PROTEASE) PROTHROMBIN FRAGMENT 1 (RESIDUES 1 - 156) COMPLEX WITH 2PF2 3 CALCIUM 2PF2 4	
916	2sta	E	11	247	2.8e-95			184.42	TRYPSIN; CHAIN: E; TRYPSIN INHIBITOR; CHAIN: 1	HYDROLASE/HYDROLASE INHIBITOR SERINE PROTEINASE, TRYPSIN INHIBITOR
916	2sta	E	445	681	1.4e-95			187.74	TRYPSIN; CHAIN: E; TRYPSIN INHIBITOR; CHAIN: 1	HYDROLASE/HYDROLASE INHIBITOR SERINE PROTEINASE, TRYPSIN INHIBITOR
916	2sta	E	445	682	1.4e-95	0.96	1.00		TRYPSIN; CHAIN: E; TRYPSIN INHIBITOR; CHAIN: 1	HYDROLASE/HYDROLASE INHIBITOR SERINE PROTEINASE, TRYPSIN INHIBITOR
916	3ktiv		10	92	4.2e-32			75.13	APOLIPROTEIN; CHAIN: NULL;	KRINGLE KRINGLE, LYSINE BINDING SITE, APOLIPROTEIN(A)
916	3ktiv		285	367	4.2e-29	0.34	1.00		APOLIPROTEIN; CHAIN: NULL;	KRINGLE KRINGLE, LYSINE BINDING SITE,

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
916	3kiv		77	153	2.8e-21	0.16	-0.09		APOLIPROTEIN; CHAIN: NULL;	APOLIPROTEIN(A) KRINGLE KRINGLE, LYSINE BINDING SITE,
916	5hpg	A	10	95	1.3e-25			67.77	PLASMINOGEN; CHAIN: A, B;	SERINE PROTEASE SERINE PROTEASE, KRINGLE 5, HUMAN PLASMINOGEN, FIBRINOLYSIS
916	5ptp		11	248	4.2e-92			185.89	BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
916	5ptp		445	682	7e-93	0.89	1.00		BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
916	5ptp		445	682	7e-93			188.52	BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
917	1d4v	A	903	1026	3e-14	0.10	-1202.08		TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	APOPTOSIS TRAIL; DR5; LIGAND- RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
917	1d4v	A	959	1075	3e-14	0.12	-1202.08		TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	APOPTOSIS TRAIL; DR5; LIGAND- RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
917	1emm		452	510	2.8e-09	0.19	-1202.08		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
917	1ext	A	280	475	1.5e-19	0.04	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
917	1ext	A	819	990	4.5e-24	0.24	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
917	1ext	A	867	1054	7.5e-25	0.25	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
917	1g40	A	786	1028	6e-20	0.29	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B;	IMMUNE SYSTEM BETA, MODULE
917	1g40	A	815	1085	1.5e-21	0.00	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B;	IMMUNE SYSTEM BETA, MODULE
917	1g44	A	780	916	1.5e-12	0.08	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
917	1g44	B	786	1095	1.5e-19	0.14	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
917	1g44	B	925	1140	1.2e-21	-0.00	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
917	1g44	B	984	1143	4.5e-14	0.02	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
917	1g44	C	877	1140	3e-18	0.10	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
917	1igr	A	218	554	1.4e-33	0.19	-1202.08		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
917	1igr	A	781	1128	7.5e-30	0.19	-1202.08		INSULIN-LIKE GROWTH	HORMONE RECEPTOR HORMONE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
917	1kdo		1051	1193	2.8e-15	0.13	-1202.08		FACTOR RECEPTOR 1; CHAIN: A;	RECEPTOR, INSULIN RECEPTOR FAMILY
917	1kdo		282	470	1.5e-33	0.29	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		294	462	5.6e-24	0.15	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		349	520	1.5e-32	0.37	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		365	519	2.8e-26	0.35	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		412	561	4.5e-29	0.44	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		424	569	1.3e-24	0.43	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		472	624	1.4e-17	0.23	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		786	925	1.4e-24	0.75	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		834	985	4.5e-28	0.61	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		839	986	2.8e-26	0.60	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		924	1099	3e-38	0.68	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		928	1091	2.8e-30	0.28	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1kdo		987	1139	2.8e-26	0.57	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
917	1ncf	A	819	967	3e-14	0.11	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	SIGNALING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19
917	1ncf	A	911	1071	1.5e-17	0.19	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	SIGNALING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19
917	1pp2	L	413	558	1.5e-09	0.01	-1202.08		HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2= (E.C.3.1.1.4) 1PP2 4	
917	1qub	A	414	569	7.5e-12	0.36	-1202.08		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2-N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
917	1qub	A	802	1116	7.5e-29	0.25	-1202.08		HUMAN BETA2-	MEMBRANE ADHESION SHORT

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									GLYCOPROTEIN I; CHAIN: A;	CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
917	1skz		1036	1142	1.5e-14	0.06	-1202.08		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
917	1skz		346	476	3e-15	0.08	-1202.08		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
917	1skz		409	526	3e-16	-0.00	-1202.08		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
917	1skz		786	882	1.5e-17	0.13	-1202.08		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
917	1skz		830	931	1.1e-15	0.75	-1202.08		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
917	1skz		877	989	6e-14	0.26	-1202.08		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
917	1skz		984	1097	3e-11	0.09	-1202.08		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
917	1tle		282	349	9e-11	0.21	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN LAMININ-TYPE EGF-LIKE; GLYCOPROTEIN, EXTRACELLULAR MATRIX PROTEIN, NIDOGEN BINDING, 2 LE-MODULE
917	1tle		411	472	1.2e-09	0.17	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN LAMININ-TYPE EGF-LIKE; GLYCOPROTEIN, EXTRACELLULAR MATRIX PROTEIN, NIDOGEN BINDING, 2 LE-MODULE
917	9wga	A	1002	1195	4.2e-15	0.13	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLLECTIN 2) 9WGA 3	
917	9wga	A	311	526	1.5e-16	0.12	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLLECTIN 2) 9WGA 3	
917	9wga	A	370	554	7e-13	0.28	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLLECTIN 2) 9WGA 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
917	9wga	A	376	556	1.5e-23	0.30	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
917	9wga	A	425	608	2.8e-14	0.21	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
917	9wga	A	453	650	1.4e-13	0.12	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
917	9wga	A	793	978	5.6e-12	0.44	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
917	9wga	A	798	989	3e-20	0.22	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
917	9wga	A	863	1081	1.5e-19	0.06	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
918	lapq		27	69	1e-10	0.27	-1202.08		COMPLEMENT PROTEASE C1R; CHAIN: NULL;	COMPLEMENT, EGF, CALCIUM BINDING, SERINE PROTEASE
918	lant	L	29	124	1.1e-21	0.28	-1202.08		ACTIVATED PROTEIN C ₃ CHAIN: C ₁ ; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
918	1aut	L	323	415	1.5e-19	0.12	-1202.08		ACTIVATED PROTEIN C; CHAIN: C, I; D-PHE-PRO- MAI; CHAIN: P;	COAGULATION/INHIBITOR)
918	1b69		284	407	1.1e-25	0.36	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE HYDROLASE, PHOSPHOLIPASE A2, PLATELET AGGREGATION INHIBITOR, 2 PBPB HEADER MODRES
918	1dan	L	217	330	7.5e-28	0.05	-1202.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D- PHE-PHE-ARG- CHLOROMETHYLKETONE (DPRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO- FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
918	1dan	L	29	125	3e-23	0.58	-1202.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D- PHE-PHE-ARG- CHLOROMETHYLKETONE (DPRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO- FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
918	1dan	L	364	460	1.4e-09	0.36	-1202.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D- PHE-PHE-ARG- CHLOROMETHYLKETONE	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO- FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
918	1dan	L	7	119	1.3e-14	0.00	-1202.08		NE (DFFRCMK) WITH CHAIN: C; BLOOD COAGULATION FACTOR VIIA: CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
918	1dqb	A	67	151	4.5e-24	0.03	-1202.08		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
918	1dva	L	28	123	7.5e-23	0.22	-1202.08		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
918	1dva	L	364	460	1.4e-09	0.50	-1202.08		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
918	1dx5	I	112	243	9e-19	0.38	-1202.08		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL ID score	Compound	PDB annotation
918	1dx5	I	165	282	3e-19	0.75	-1202.08		CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H; THROMBIN LIGHT	PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
									THROMBIN LIGHT CHAIN: CHAIN: A, B, C, D: THROMBIN HEAVY CHAIN: CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
918	1dx5	I	283	404	9.8e-20	0.17	-1202.08		THROMBIN LIGHT CHAIN: CHAIN: A, B, C, D: THROMBIN HEAVY CHAIN: CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
									THROMBIN LIGHT CHAIN: CHAIN: A, B, C, D: THROMBIN HEAVY CHAIN: CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
918	1dx5	I	28	147	4.2e-15	0.06	-1202.08		THROMBIN LIGHT CHAIN: CHAIN: A, B, C, D: THROMBIN HEAVY CHAIN: CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
									THROMBIN LIGHT CHAIN: CHAIN: A, B, C, D: THROMBIN HEAVY CHAIN: CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
918	1emm		28	88	3e-17	0.38	-1202.08		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
918	1esl		28	142	3e-14	0.03	-1202.08		CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1- 157) 1ESL 3 (FORMERLY KNOWN AS ELAM-1) 1ESL 4	SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILIN-1 FRAGMENT, MATRIX PROTEIN
918	1ext	A	24	92	1.5e-11	0.16	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
918	1ext	A	33	189	1e-30	0.08	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
918	1ext	A	57	219	1.5e-27	0.50	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
918	1fte	A	29	74	1.5e-12	0.31	-1202.08		BLOOD COAGULATION FACTOR VII; CHAIN: A;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTTING
918	1fak	L	28	125	1.5e-23	0.51	-1202.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO- FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
918	1fak	L	321	410	1.1e-20	0.14	-1202.08		BLOOD COAGULATION	BLOOD CLOTTING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verity score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR VIIA; CHAIN: I; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO- FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
918	1fak	L	364	460	1.4e-09	0.32	-1202.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: I; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO- FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
918	1g40	A	151	393	3e-21	0.28	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B;	IMMUNE SYSTEM BETA, MODULE
918	1g40	A	68	275	1.5e-23	0.02	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B;	IMMUNE SYSTEM BETA, MODULE
918	1g44	A	119	314	7.5e-18	0.28	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
918	1g44	B	46	282	1.5e-28	0.02	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
918	1g44	C	110	314	4.5e-18	0.12	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
918	1hj7	A	161	243	7.5e-17	0.17	-1202.08		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
918	1hj7	A	286	356	1.5e-26	0.12	-1202.08		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
918	1hj7	A	31	110	6e-24	0.31	-1202.08		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
918	1hj7	A	327	404	6e-22	0.30	-1202.08		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
918	1hj7	A	72	151	1.5e-25	0.36	-1202.08		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
918	1igr	A	56	400	7.5e-37	0.10	-1202.08		INSULIN-LIKE GROWTH FACTOR RECEPTOR I; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
918	1kig	L	247	295	4.5e-17	0.02	-1202.08		FACTOR XA; CHAIN: H; I; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
918	1kdo		507	650	2.8e-09	0.04	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
918	1pfx	L	210	348	1.5e-21	0.06	-1202.08		FACTOR IXA; CHAIN: C ₂ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
918	1pfx	L	364	460	1.4e-09	0.45	-1202.08		FACTOR IXA; CHAIN: C ₂ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
918	1pfx	L	44	185	4.5e-25	0.02	-1202.08		FACTOR IXA; CHAIN: C ₂ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
918	1pfx	L	6	119	2.8e-11	0.05	-1202.08		FACTOR IXA; CHAIN: C ₂ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
918	1qfk	L	368	460	2.8e-08	0.54	-1202.08		COAGULATION FACTOR VIIA (LIGHT CHAIN);	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: L; COAGULATION FACTOR VIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	PROTEASE
918	1qub	A	240	480	7.5e-20	0.11	-1202.08		HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
918	1sfp		704	817	3e-21	0.72	-1202.08		ASFP; CHAIN: NULL;	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X- RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
918	1sfp		705	822	1.4e-08	0.84	-1202.08		ASFP; CHAIN: NULL;	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X- RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
918	1spp	A	708	817	6e-21	0.16	-1202.08		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B	COMPLEX (SEMINAL PLASMA PROTEIN/SP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SP)
918	1spp	B	708	821	1.2e-23	0.17	-1202.08		MAJOR SEMINAL	COMPLEX (SEMINAL PLASMA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
918	1vap	A	285	407	1e-24	0.13	-1202.08		PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B	PROTEIN/SP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SP)
918	9wga	A	361	540	1.4e-13	0.17	-1202.08		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
918	9wga	A	393	552	2.8e-14	0.19	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
918	9wga	A	435	591	1.4e-15	0.25	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
920	1ae7		239	367	9e-18	0.12	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE PLA2, PHOSPHATIDE SN-2 ACYLHYDROLASE; HYDROLASE, PHOSPHOLIPASE A2, LIPID DEGRADATION, PRESTYNAPTIC 2 NEUROTOXIN, VENOM
920	1ae7		275	395	7.5e-19	0.12	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE PLA2, PHOSPHATIDE SN-2 ACYLHYDROLASE; HYDROLASE, PHOSPHOLIPASE A2, LIPID DEGRADATION, PRESTYNAPTIC 2 NEUROTOXIN, VENOM
920	1aut	L	10	123	8.4e-10			54.46	ACTIVATED PROTEIN C ₂	COMPLEX (BLOOD

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL ID score	Compound	PDB annotation
									CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
920	1aut	L	1	96	5.6e-17			58.42	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
920	1aut	L	223	333	1.5e-16	0.57	-1202.08		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
920	1aut	L	252	367	1e-14	0.07	-1202.08		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
920	1aut	L	295	409	6e-13	0.45	-1202.08		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
920	1aut	L	79	165	1.2e-22	0.54	-1202.08		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
920	1aut	L	8	108	1.4e-21			65.70	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
920	1aut	L	8	95	4.5e-21	0.13	-1202.08		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
920	1bk9		124	270	6e-09	0.08	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE HYDROLASE, PHOSPHOLIPASE A2, PLATELET AGGREGATION INHIBITOR, 2 PBPB HEADER MODRES
920	1bk9		239	354	9e-18	0.01	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE HYDROLASE, PHOSPHOLIPASE A2, PLATELET AGGREGATION INHIBITOR, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
920	1bk9		44	154	6e-21	0.21	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	BBPB HEADER MODRES HYDROLASE HYDROLASE, PHOSPHOLIPASE A2, PLATELET AGGREGATION INHIBITOR, 2 BBPB HEADER MODRES
920	1clg	A	185	452	1.3e-11			67.87	TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
920	1clg	A	24	304	4.2e-13			65.53	TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
920	1c2a	A	10	147	2.8e-06			61.18	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
920	1c2a	A	280	430	1.5e-11	0.51	-1202.08		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
920	1dan	L	1	110	1.3e-22			54.26	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
920	1dan	L	252	411	7.5e-15	0.12	-1202.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PME score	SEQFOL ID score	Compound	PDB annotation
									H, I; DES-GLA FACTOR VILA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	COMPLEX
920	1dva	L	363	448	4.2e-12	0.34	-1202.08		DES-GLA FACTOR VILA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VILA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
								52.84	DES-GLA FACTOR VILA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VILA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
920	1dva	L	81	168	1.5e-22	0.28	-1202.08		DES-GLA FACTOR VILA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VILA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
920	1dva	L	8	98	4.5e-18	0.23	-1202.08		DES-GLA FACTOR VILA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VILA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
920	1dva	L	9	110	1.3e-22			69.15	ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y; DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
920	1dx5	I	1	103	7e-18			54.30	THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
920	1dx5	I	1	129	1.1e-12			52.74	THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
920	1dx5	I	231	353	6e-16	0.18	-1202.08		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
920	1dx5	I	41	163	7.5e-25	0.43	-1202.08		THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
									THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
920	1dx5	I	8	112	4.2e-15	0.50	-1202.08		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
920	1dx5	I	8	122	1.4e-26	0.69	-1202.08		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
920	1emm		10	93	8.4e-20			71.76	FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY,

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
920	1enn		1	82	2.8e-17			52.08	FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
920	1enn		358	434	9.8e-16	0.30	-1202.08		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
920	1esl		252	395	9e-16	0.19	-1202.08		CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1-157) 1ESL 3 (FORMERLY KNOWN AS ELAM-1) 1ESL 4	
920	1esl		280	439	7.5e-15	0.33	-1202.08		CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1-157) 1ESL 3 (FORMERLY KNOWN AS ELAM-1) 1ESL 4	
920	1ext	A	223	389	6e-26	0.50	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR,	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
920	1ext	A	23	168	3e-29	0.55	-1202.08		CHAIN: A, B; TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
920	1ext	A	282	451	3e-19	0.42	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
920	1ext	A	68	258	3e-22	0.09	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
920	1ext	A	8	141	1.5e-25	0.17	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
920	1fak	L	223	331	1.5e-13	0.39	-1202.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX/SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4
										PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
920	1fak	L	279	367	3e-12	0.27	-1202.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX/SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4
										PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
920	1fak	L	363	448	4.2e-12	0.26	-1202.08		BLOOD COAGULATION	BLOOD CLOTTING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO- FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
920	1fak	L	76	168	3e-24	0.20	-1202.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO- FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
920	1fak	L	8	100	9e-20	0.20	-1202.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO- FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
920	1fak	L	9	111	1.3e-22			63.80	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO- FACTOR, RECEPTOR ENZYME, 3

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									5L15; CHAIN: I;	INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
920	1g40	A	228	402	4.5e-19	0.21	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B;	IMMUNE SYSTEM BETA, MODULE
920	1g40	A	232	439	1.3e-25	0.12	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B;	IMMUNE SYSTEM BETA, MODULE
920	1g40	A	45	315	4.5e-19	0.09	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B;	IMMUNE SYSTEM BETA, MODULE
920	1g40	A	58	311	4.5e-19			91.21	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B;	IMMUNE SYSTEM BETA, MODULE
920	1g44	A	223	435	7.5e-24	0.02	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
920	1g44	A	67	325	1.3e-20	0.15	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
920	1g44	A	92	339	4.5e-17	0.01	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
920	1g44	B	236	452	1.5e-23	0.36	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
920	1g44	B	54	325	3e-22	0.18	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
920	1g44	B	58	311	3e-22			85.82	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
920	1g44	C	276	462	7.5e-19	0.02	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
920	1g44	C	50	314	4.5e-14	0.03	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
920	1g44	C	82	324	6e-14	0.06	-1202.08		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
920	1hj7	A	13	93	2.8e-21			79.27	LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
920	1hj7	A	1	65	7e-21			59.44	LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
920	1hj7	A	1	66	4.2e-19			56.38	LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
920	1hj7	A	1	82	2.8e-20			60.67	LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
920	1hj7	A	44	123	3e-26			92.35	LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
920	1hj7	A	45	123	3e-26	0.82	-1202.08		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
920	1hj7	A	6	82	9e-20	0.60	-1202.08		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
920	1hj7	A	86	163	3e-25	0.75	-1202.08		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
920	1igr	A	68	447	3e-32	0.02	-1202.08		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
920	1kio		15	148	1.1e-24			89.71	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
920	1kio		239	367	4.5e-27	0.50	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
920	1kio		280	413	4.5e-27			89.39	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
920	1kio		280	441	4.5e-22	0.49	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
920	1kio		323	455	1.4e-14	0.33	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
920	1kio		366	483	7e-14	0.22	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
920	1kio		77	245	5.6e-11			62.00	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
920	1nub	A	279	461	3e-13	0.00	-1202.08		BASEMENT MEMBRANE PROTEIN BM-40; CHAIN: A, B;	EXTRACELLULAR MODULE OSTEOONECTIN, SPARC, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, GLYCOPROTEIN, ANTI-ADHESIVE PROTEIN, 2 COLLAGEN BINDING, SITE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODRES

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
920	1pfx	L	18	154	2.8e-12			56.67	FACTOR IXA; CHAIN: C ₃ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
920	1pfx	L	219	340	3e-17	0.16	-1202.08		FACTOR IXA; CHAIN: C ₃ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
920	1pfx	L	2	116	4.2e-20			58.15	FACTOR IXA; CHAIN: C ₃ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
920	1pfx	L	50	165	1.5e-26	0.54	-1202.08		FACTOR IXA; CHAIN: C ₃ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
920	1pp2	L	239	355	1.5e-17	-0.00	-1202.08		HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2= (E.C.3.1.1.4) 1PP2 4	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
920	1qfk	L	16	112	4.2e-21			63.17	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
920	1qfk	L	1	96	2.8e-16			54.95	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
920	1qfk	L	363	448	4.2e-12	0.09	-1202.08		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
920	1qub	A	33	431	1.5e-26	0.06	-1202.08		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
920	1skz		11	115	1.3e-06			57.67	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
920	1skz		239	342	3e-17	0.00	-1202.08		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR;

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Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
920	1skz		279	414	1.5e-20	0.20	-1202.08		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
920	1skz		323	451	7.5e-15	0.21	-1202.08		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
920	1skz		40	150	4.2e-08			59.01	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
										PLASMINOGEN ACTIVATION
920	1tpg		223	307	1.2e-14	0.08	-1202.08		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	LIPID DEGRADATION PHOSPHOLIPASE A2; LIPID DEGRADATION, HYDROLASE
920	1vap	A	239	355	4.5e-17	0.15	-1202.08		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2; LIPID DEGRADATION, HYDROLASE
920	1vap	A	324	447	3e-13	0.27	-1202.08		PHOSPHOLIPASE A2; CHAIN: A, B;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;
920	1xka	L	16	110	9.8e-19			67.01	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										PROTEINASE, EPIDERMAL 2
920	1xka	L	1	100	1.4e-17			63.53	BLOOD COAGULATION FACTOR XA; CHAIN: L, C ₃	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2
										GROWTH FACTOR LIKE DOMAIN
920	1xka	L	276	366	6e-15	0.24	-1202.08		BLOOD COAGULATION FACTOR XA; CHAIN: L, C ₃	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2
										GROWTH FACTOR LIKE DOMAIN
920	1xka	L	7	98	1.5e-18	0.15	-1202.08		BLOOD COAGULATION FACTOR XA; CHAIN: L, C ₃	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2
										GROWTH FACTOR LIKE DOMAIN
920	1xka	L	88	165	3e-20	1.13	-1202.08		BLOOD COAGULATION FACTOR XA; CHAIN: L, C ₃	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2
										GROWTH FACTOR LIKE DOMAIN
920	9wga	A	1	150	1.4e-15			73.10	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
920	9wga	A	223	354	1.2e-20	0.48	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
920	9wga	A	232	414	1.5e-24	0.47	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
920	9wga	A	266	433	1.4e-12	0.38	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
920	9wga	A	273	448	6e-24	0.49	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
920	9wga	A	310	466	7e-14	0.29	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
920	9wga	A	47	237	9.8e-15			54.16	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
922	laye		1	301	0			301.57	PROCARBOXYPEPTIDAS E A2; CHAIN: NULL;	SERINE PROTEASE PCPA2; SERINE PROTEASE, ZYMOGEN, HYDROLASE
922	laye		1	446	0			424.65	PROCARBOXYPEPTIDAS E A2; CHAIN: NULL;	SERINE PROTEASE PCPA2; SERINE PROTEASE, ZYMOGEN, HYDROLASE
922	laye		3	446	0	0.54	-1202.08		PROCARBOXYPEPTIDAS E A2; CHAIN: NULL;	SERINE PROTEASE PCPA2; SERINE PROTEASE, ZYMOGEN, HYDROLASE
922	ldid	A	144	446	0	0.85	-1202.08		CARBOXYPEPTIDASE A2; CHAIN: A; METALLOCARBOXYPEP TIDASE INHIBITOR; CHAIN: B	HYDROLASE/HYDROLASE INHIBITOR CARBOXYPEPTIDASE A2, LEECH CARBOXYPEPTIDASE INHIBITOR
922	ldid	A	144	446	0			364.24	CARBOXYPEPTIDASE A2; CHAIN: A; METALLOCARBOXYPEP TIDASE INHIBITOR;	HYDROLASE/HYDROLASE INHIBITOR CARBOXYPEPTIDASE A2, LEECH CARBOXYPEPTIDASE INHIBITOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
922	1dtd	A	6	301	0			346.47	CHAIN: B CARBOXYPEPTIDASE A2; CHAIN: A; METALLOCARBOXYPEPTIDASE INHIBITOR; CHAIN: B	HYDROLASE/HYDROLASE INHIBITOR CARBOXYPEPTIDASE A2, LEECH CARBOXYPEPTIDASE INHIBITOR
922	1pca		1	301	0			312.30	HYDROLASE(C- TERMINAL PEPTIDASE) PROCARBOXYPEPTIDASE A (E.C.3.4.12.2) 1PCA 3	
922	1pca		1	446	0			444.93	HYDROLASE(C- TERMINAL PEPTIDASE) PROCARBOXYPEPTIDASE A (E.C.3.4.12.2) 1PCA 3	
922	2ctc		138	444	0			388.28	HYDROLASE(C- TERMINAL PEPTIDASE) CARBOXYPEPTIDASE A (E.C.3.4.17.1) COMPLEX WITH L-PHENYL 2CTC 3 LACTATE (L-O-PHE) 2CTC 4	
922	2ctc		139	444	0	0.92	-1202.08		HYDROLASE(C- TERMINAL PEPTIDASE) CARBOXYPEPTIDASE A (E.C.3.4.17.1) COMPLEX WITH L-PHENYL 2CTC 3 LACTATE (L-O-PHE) 2CTC 4	
922	2ctc		1	301	0			376.85	HYDROLASE(C- TERMINAL PEPTIDASE) CARBOXYPEPTIDASE A (E.C.3.4.17.1) COMPLEX WITH L-PHENYL 2CTC 3 LACTATE (L-O-PHE) 2CTC 4	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
927	1bkt		1	92	9.8e-32			61.12	FK506 BINDING PROTEIN; CHAIN: NULL;	ISOMERASE FKBP; ISOMERASE, ROTAMASE
927	1bkt		30	125	1.4e-31			68.15	FK506 BINDING PROTEIN; CHAIN: NULL;	ISOMERASE FKBP; ISOMERASE, ROTAMASE
927	1bkt		34	125	1.4e-31	0.49	0.96		FK506 BINDING PROTEIN; CHAIN: NULL;	ISOMERASE FKBP; ISOMERASE, ROTAMASE
927	1c9h	A	30	125	1.4e-33			53.32	FKBP12.6; CHAIN: A;	IMMUNE SYSTEM CALCINEURIN; FKBP12, RAPAMYCIN, COMPLEX, RYANODINE RECEPTOR
927	1c9h	A	34	125	1.4e-33	0.47	0.92		FKBP12.6; CHAIN: A;	IMMUNE SYSTEM CALCINEURIN; FKBP12, RAPAMYCIN, COMPLEX, RYANODINE RECEPTOR
927	1c9h	A	34	125	2.8e-28	0.50	0.76		FKBP12.6; CHAIN: A;	IMMUNE SYSTEM CALCINEURIN; FKBP12, RAPAMYCIN, COMPLEX, RYANODINE RECEPTOR
927	1fd9	A	16	126	4.2e-35	0.21	0.15		MACROPHAGE INFECTIVITY POTENTIATOR PROTEIN; CHAIN: A;	ISOMERASE MIP, PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, PIASE, FKBP DOMAIN, LONG ALPHA HELIX, DIMERISATION VIA HELICAL 2 INTERACTIONS
927	1fd9	A	26	126	8.5e-32	0.52	0.64		MACROPHAGE INFECTIVITY POTENTIATOR PROTEIN; CHAIN: A;	ISOMERASE MIP, PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, PIASE, FKBP DOMAIN, LONG ALPHA HELIX, DIMERISATION VIA HELICAL 2 INTERACTIONS
927	1pbk		1	92	2.8e-26			59.85	FKBP25; CHAIN: NULL;	ISOMERASE FKBP25 C-TERMINAL DOMAIN; FKBP12 HOMOLOGOUS DOMAIN OF HFKBP25, ISOMERASE
927	1pbk		29	125	1e-31			65.99	FKBP25; CHAIN: NULL;	ISOMERASE FKBP25 C-TERMINAL DOMAIN; FKBP12 HOMOLOGOUS DOMAIN OF HFKBP25, ISOMERASE
927	1pbk		30	125	1e-31	0.73	0.99		FKBP25; CHAIN: NULL;	ISOMERASE FKBP25 C-TERMINAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
927	1rot		24	125	5.1e-33	0.50	0.98		FKBP59-I; CHAIN: NULL;	DOMAIN; FKBP12 HOMOLOGOUS DOMAIN OF HFKBP25, ISOMERASE
927	1rot		24	126	5.1e-33			60.50	FKBP59-I; CHAIN: NULL;	ROTAMASE (ISOMERASE) FKBP52 OR HSP56; ROTAMASE (ISOMERASE), DOMAIN I (N-TERM) OF A 59 KDA, 2 FK506-BINDING PROTEIN, PEPTIDYL PROLYL CIS-TRANS ISOMERASE
927	1rot		26	125	1.4e-32	0.53	0.92		FKBP59-I; CHAIN: NULL;	ROTAMASE (ISOMERASE) FKBP52 OR HSP56; ROTAMASE (ISOMERASE), DOMAIN I (N-TERM) OF A 59 KDA, 2 FK506-BINDING PROTEIN, PEPTIDYL PROLYL CIS-TRANS ISOMERASE
927	1yat		1	92	4.2e-30			63.65	BINDING PROTEIN FK-506 BINDING PROTEIN (12 KD, YEAST) COMPLEX WITH 1YAT 3	
927	1yat		21	124	5.1e-33	0.55	0.99		BINDING PROTEIN FK-506 BINDING PROTEIN (12 KD, YEAST) COMPLEX WITH 1YAT 3	
927	1yat		22	125	5.1e-33			72.40	BINDING PROTEIN FK-506 BINDING PROTEIN (12 KD, YEAST) COMPLEX WITH 1YAT 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
927	1yat		31	124	2.8e-30	0.32	0.94		FK-506 1YAT 4	
									BINDING PROTEIN FK-506 BINDING PROTEIN (12 KD, YEAST) COMPLEX WITH 1YAT 3 FK-506 1YAT 4	
930	1dii	A	173	647	2.8e-55			144.75	P-CRESOL METHYLHYDROXYLAS E; CHAIN: A, B; P-CRESOL METHYLHYDROXYLAS E; CHAIN: C, D;	OXIDOREDUCTASE PCMH; PCMH; FLAVOCYTOCHROME, ELECTRON-TRANSFER, FAD, HEME
930	1e8g	A	167	647	5.6e-45			137.59	VANILLYL-ALCOHOL OXIDASE; CHAIN: A, B;	OXIDOREDUCTASE ARYL-ALCOHOL OXIDASE, 4-ALLYLPHENOL OXIDASE; FLAVOENZYME, SPECIFICITY
930	1f0x	A	182	648	5.6e-27			84.21	D-LACTATE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE DLDH; OXIDOREDUCTASE
935	1lba		401	546	1.5e-47	0.57	0.70		HYDROLASE(ACTING ON LINEAR AMIDES) LYSOZYME (E.C.3.5.1.28) MUTANT WITH ALA 6 REPLACED BY LYS ILBA 3 AND RESIDUES 2-5 DELETED (DEL(2-5),A6K) ILBA 4	
935	1lba		429	542	2.8e-25	0.39	0.96		HYDROLASE(ACTING ON LINEAR AMIDES) LYSOZYME (E.C.3.5.1.28) MUTANT WITH ALA 6 REPLACED BY LYS ILBA 3 AND RESIDUES 2-5 DELETED (DEL(2-5),A6K) ILBA 4	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
937	14ps	B	1	231	0			251.78	14-3-3 PROTEIN ZETA/DELTA; CHAIN: A, B; PHOSHOPEPTIDE; CHAIN: Q, R;	COMPLEX (NEURONE/PEPTIDE) COMPLEX (NEURONE/PEPTIDE), 14-3-3, PHOSHOPEPTIDE, 2 SIGNAL TRANSDUCTION
937	14ps	B	43	278	0			250.78	14-3-3 PROTEIN ZETA/DELTA; CHAIN: A, B; PHOSHOPEPTIDE; CHAIN: Q, R;	COMPLEX (NEURONE/PEPTIDE) COMPLEX (NEURONE/PEPTIDE), 14-3-3, PHOSHOPEPTIDE, 2 SIGNAL TRANSDUCTION
937	14ps	B	53	278	0	0.56	1.00		14-3-3 PROTEIN ZETA/DELTA; CHAIN: A, B; PHOSHOPEPTIDE; CHAIN: Q, R;	COMPLEX (NEURONE/PEPTIDE) COMPLEX (NEURONE/PEPTIDE), 14-3-3, PHOSHOPEPTIDE, 2 SIGNAL TRANSDUCTION
937	14ps	B	58	277	6.8e-96	0.56	1.00		14-3-3 PROTEIN ZETA/DELTA; CHAIN: A, B; PHOSHOPEPTIDE; CHAIN: Q, R;	COMPLEX (NEURONE/PEPTIDE) COMPLEX (NEURONE/PEPTIDE), 14-3-3, PHOSHOPEPTIDE, 2 SIGNAL TRANSDUCTION
937	1440	A	1	227	4.2e-90			180.87	14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	SIGNAL TRANSDUCTION SIGNAL
937	1440	A	43	274	1.4e-90			180.40	14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	SIGNAL TRANSDUCTION SIGNAL
937	1440	A	53	274	1.4e-90	0.54	1.00		14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	SIGNAL TRANSDUCTION SIGNAL
937	14ja	A	1	229	0			227.29	14-3-3 PROTEIN ZETA; CHAIN: A, B; PHOSHOPEPTIDE; CHAIN: Q, R	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX, 14-3-3, PHOSHOPEPTIDE, SIGNAL TRANSDUCTION
937	14ja	A	43	276	0			226.45	14-3-3 PROTEIN ZETA; CHAIN: A, B; PHOSHOPEPTIDE; CHAIN: Q, R	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX, 14-3-3, PHOSHOPEPTIDE, SIGNAL TRANSDUCTION
937	14ja	A	53	276	0	0.51	1.00		14-3-3 PROTEIN ZETA; CHAIN: A, B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PHOSPHOPEPTIDE; CHAIN: Q, R	COMPLEX, 14-3-3, PHOSHOPEPTIDE, SIGNAL TRANSDUCTION
938	1a4p	A	63	150	8.5e-31	0.80	1.00		S100A10; CHAIN: A, B;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN P11, CALPACTIN LIGHT CHAIN; S100 FAMILY, EF-HAND PROTEIN, LIGAND OF ANNEXIN II, 2 CALCIUM/PHOSPHOLIPID BINDING PROTEIN
938	1a4p	A	63	153	8.5e-31			69.95	S100A10; CHAIN: A, B;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN P11, CALPACTIN LIGHT CHAIN; S100 FAMILY, EF-HAND PROTEIN, LIGAND OF ANNEXIN II, 2 CALCIUM/PHOSPHOLIPID BINDING PROTEIN
938	1b4c	A	1	87	2.8e-22			135.96	S-100 PROTEIN, BETA CHAIN; CHAIN: A, B;	METAL BINDING PROTEIN S100B, S100BETA; S100BETA, S100B, NMR, DIPOLAR COUPLINGS, EF-HAND, S100 2 PROTEIN, CALCIUM- BINDING PROTEIN, FOUR-HELIX BUNDLE, THREE-3 DIMENSIONAL STRUCTURE, SOLUTION STRUCTURE
938	1b4c	A	62	153	4.2e-29	0.61	1.00		S-100 PROTEIN, BETA CHAIN; CHAIN: A, B;	METAL BINDING PROTEIN S100B, S100BETA; S100BETA, S100B, NMR, DIPOLAR COUPLINGS, EF-HAND, S100 2 PROTEIN, CALCIUM- BINDING PROTEIN, FOUR-HELIX BUNDLE, THREE-3 DIMENSIONAL STRUCTURE, SOLUTION STRUCTURE
938	1b4c	A	62	153	4.2e-29			145.34	S-100 PROTEIN, BETA CHAIN; CHAIN: A, B;	METAL BINDING PROTEIN S100B, S100BETA; S100BETA, S100B,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										NMR, DIPOLAR COUPLINGS, EF-HAND, S100 2 PROTEIN, CALCIUM-BINDING PROTEIN, FOUR-HELIX BUNDLE, THREE-3 DIMENSIONAL STRUCTURE, SOLUTION STRUCTURE
938	1e8a	A	63	148	1.2e-33	0.71	1.00		S100A12; CHAIN: A, B;	S100 PROTEIN CALGRANULIN C S100 PROTEIN, X-RAY STRUCTURE, EF-HAND, CALCIUM BINDING
938	1e8a	A	63	149	1.2e-33			76.74	S100A12; CHAIN: A, B;	S100 PROTEIN CALGRANULIN C S100 PROTEIN, X-RAY STRUCTURE, EF-HAND, CALCIUM BINDING
938	1g8i	A	49	139	3.4e-07	-0.11	0.27		NEURONAL CALCIUM SENSOR 1; CHAIN: A, B;	METAL BINDING PROTEIN FREQUENIN; CALCIUM BINDING-PROTEIN, EF-HAND, CALCIUM ION
938	1iku		49	139	1.7e-06	0.41	0.23		RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
938	1mho		1	87	2.8e-22			134.69	S-100 PROTEIN; CHAIN: NULL;	CALCIUM-BINDING CALCIUM-BINDING, ZINC, METAL-BINDING, ACETYLATION
938	1mho		63	150	1.7e-27	0.71	1.00		S-100 PROTEIN; CHAIN: NULL;	CALCIUM-BINDING CALCIUM-BINDING, ZINC, METAL-BINDING, ACETYLATION
938	1mho		63	150	1.7e-27			137.44	S-100 PROTEIN; CHAIN: NULL;	CALCIUM-BINDING CALCIUM-BINDING, ZINC, METAL-BINDING, ACETYLATION
938	1mho		63	150	4.2e-27	0.71	1.00		S-100 PROTEIN; CHAIN: NULL;	CALCIUM-BINDING CALCIUM-BINDING, ZINC, METAL-BINDING, ACETYLATION
938	1mr8	A	61	153	8.5e-31			62.97	MIGRATION	METAL TRANSPORT MRP8,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									INHIBITORY FACTOR-RELATED PROTEIN 8; CHAIN: A, B;	S100A8, CALGRANULIN A CALCIUM-BINDING PROTEIN, CRYSTAL STRUCTURE, MAD, MIGRATION 2 INHIBITORY FACTOR, RELATED PROTEIN 8, S100 PROTEIN
938	1mr8	A	62	153	8.5e-31	0.24	0.75		MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 8; CHAIN: A, B;	METAL TRANSPORT MRP8, S100A8, CALGRANULIN A CALCIUM-BINDING PROTEIN, CRYSTAL STRUCTURE, MAD, MIGRATION 2 INHIBITORY FACTOR, RELATED PROTEIN 8, S100 PROTEIN
938	1qls	A	63	150	1e-34	0.39	0.99		S100C PROTEIN; CHAIN: A; ANNEXIN I; CHAIN: D;	COMPLEX (LIGAND/ANNEXIN) CALGIZZARIN; S100 FAMILY, EF-HAND PROTEIN, COMPLEX (LIGAND/ANNEXIN), 2 LIGAND OF ANNEXIN II, CALCIUM/PHOSPHOLIPID BINDING PROTEIN
								80.67	S100C PROTEIN; CHAIN: A; ANNEXIN I; CHAIN: D;	COMPLEX (LIGAND/ANNEXIN) CALGIZZARIN; S100 FAMILY, EF-HAND PROTEIN, COMPLEX (LIGAND/ANNEXIN), 2 LIGAND OF ANNEXIN II, CALCIUM/PHOSPHOLIPID BINDING PROTEIN
938	1qls	A	63	153	1e-34					
940	12e8	H	133	310	9.8e-27	0.28	0.09		2E8 (IGG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
940	12e8	H	313	504	5.6e-58	0.25	0.04		2E8 (IGG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
940	1a0q	H	25	220	1.1e-67	0.32	0.55		29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
940	1ad0	B	25	220	2.8e-68	0.16	0.33		FAB FRAGMENT, ANTIBODY A5B7; CHAIN: A, B, C, D; ANTIBODY CTM01; CHAIN: L, H;	ESTERASE IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
940	1ae6	H	24	219	2.8e-67	0.38	0.35		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
940	1afv	H	24	221	2.8e-70	0.21	-0.01		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
940	1afv	H	312	503	2.8e-56	0.30	-0.08		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
940	1ai1	L	128	307	4.2e-25	0.37	0.49		FAB59.1; CHAIN: L, H; AIB142; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE) COMPLEX (ANTIBODY/PEPTIDE), ANTIBODY, CONSTRAINED HIV-1 V3 2 LOOP PEPTIDE, IMMUNOGLOBULIN
940	1aif	A	128	311	4.2e-26	0.21	-0.02		ANTI-IDiotYPIC FAB 409.5.3 (GG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
940	1aif	B	25	219	1.4e-66	0.08	-0.07		ANTI-IDiotYPIC FAB 409.5.3 (GG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
940	1b2w	H	25	221	2.8e-69	0.15	0.00		ANTIBODY (LIGHT CHAIN); CHAIN: L;	IMMUNE SYSTEM IMMUNOGLOBULIN;

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
940	1b2w	L	128	311	5.6e-26	0.34	-0.03		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
940	1b6d	A	128	307	2.8e-25	0.22	0.11		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
940	1b1j	H	25	219	2.8e-67	0.19	0.16		IMMUNOGLOBULIN FAB FRAGMENT OF MONOCLONAL ANTIBODY B72.3 1BBJ 3 (MURINE/HUMAN CHIMERA) 1BBJ 4	
940	1b1h	A	126	500	3.4e-42	0.55	0.87		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
940	1b1h	A	227	611	8.4e-25	0.27	-0.06		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
940	1b1h	A	22	396	1.4e-50			125.54	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
940	1b1h	A	24	396	1.4e-50	0.34	0.89		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
940	1b1j	J	128	310	5.6e-26	0.10	0.09		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
940	1b1n	B	25	221	1.1e-69	-0.06	0.22		MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN: A, C; MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM
940	1c5c	H	24	221	2.8e-69	0.22	0.60		CHIMERIC DECARBOXYLASE ANTIBODY 21D8; CHAIN: L; CHIMERIC DECARBOXYLASE ANTIBODY 21D8; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN, CATALYTIC ANTIBODY, CHIMERIC FAB, 2 DECARBOXYLASE, HAPTEN COMPLEX
940	1c1c	B	24	221	8.4e-70	0.50	0.41		IG HEAVY CHAIN V REGIONS; CHAIN: A; IG HEAVY CHAIN V REGIONS; CHAIN: B; IG HEAVY CHAIN V REGIONS; CHAIN: C; IG HEAVY CHAIN V REGIONS; CHAIN: D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB COMPLEX, IDIOTOPE, ANTI-IDIOTOPE
940	1c1c	B	312	503	4.2e-57	0.27	0.18		IG HEAVY CHAIN V REGIONS; CHAIN: A; IG HEAVY CHAIN V REGIONS; CHAIN: B; IG	IMMUNOGLOBULIN, FAB COMPLEX, IDIOTOPE, ANTI-IDIOTOPE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HEAVY CHAIN V REGIONS; CHAIN: C; IG HEAVY CHAIN V REGIONS; CHAIN: D;	
940	1cl7	I	140	222	4.2e-26	0.60	0.12		IGG1 ANTIBODY 1696 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 1696 (VARIABLE HEAVY CHAIN); CHAIN: H; IGG1 ANTIBODY 1696 (CONSTANT HEAVY CHAIN); CHAIN: I;	IMMUNE SYSTEM IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1 FAB FRAGMENT, CROSS-REACTIVITY, HIV1 PROTEASE, ENZYME 2 INHIBITION, IMMUNOGLOBULIN
940	1cl7	I	413	505	4.2e-28	0.10	-0.13		IGG1 ANTIBODY 1696 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 1696 (VARIABLE HEAVY CHAIN); CHAIN: H; IGG1 ANTIBODY 1696 (CONSTANT HEAVY CHAIN); CHAIN: I;	IMMUNE SYSTEM IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1 FAB FRAGMENT, CROSS-REACTIVITY, HIV1 PROTEASE, ENZYME 2 INHIBITION, IMMUNOGLOBULIN
940	1cf9	H	136	309	2.8e-25	0.11	0.22		FAB ANTIBODY LIGHT CHAIN; CHAIN: L; FAB ANTIBODY HEAVY CHAIN; CHAIN: H;	IMMUNE SYSTEM ANTI-PRION FAB 3F4; ANTI-PRION FAB 3F4 ANTI-PRION ANTIBODY, FAB 3F4
									AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
940	1cs6	A	122	500	1.7e-47	0.26	1.00		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
940	1cs6	A	122	504	1.7e-47			129.23	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
940	1cs6	A	132	503	1.1e-35	0.27	0.07		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
940	1cs6	A	225	611	2.8e-35	0.21	0.27		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
940	1cs6	A	24	392	2.8e-64	0.15	0.63		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
940	1ct8	A	128	311	4.2e-25	0.36	0.07		7C8 FAB FRAGMENT; SHORT CHAIN; CHAIN: A, C; 7C8 FAB FRAGMENT; LONG CHAIN; CHAIN: B, D	IMMUNE SYSTEM ABZYME TRANSITION STATE ANALOG, IMMUNE SYSTEM
940	1ct8	B	312	505	1.4e-56	0.18	0.31		7C8 FAB FRAGMENT; SHORT CHAIN; CHAIN: A, C; 7C8 FAB FRAGMENT; LONG CHAIN; CHAIN: B, D	IMMUNE SYSTEM ABZYME TRANSITION STATE ANALOG, IMMUNE SYSTEM
940	1dee	A	128	311	9.8e-27	0.24	0.18		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H; IMMUNOGLOBULIN 3D6 FAB 1DFB 3	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
940	1dfb	L	128	311	2.8e-26	0.03	0.01		IMMUNOGLOBULIN 3D6 FAB 1DFB 3	
940	1dgi	R	132	396	5.1e-32	0.18	0.45		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
940	1dgi	R	223	500	1.7e-23	-0.21	0.00		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
940	1dgi	R	25	308	1e-45			126.61	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: 3; VP4; CHAIN: 4;	MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
940	1dgi	R	26	308	1e-45	-0.16	0.03		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
940	1dh2	A	144	303	9.8e-31	0.06	0.59		IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A; B; ENGINEERED PEPTIDE; CHAIN: E, F;	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE
940	1dh2	A	227	393	4.2e-37	0.22	-0.01		IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A; B; ENGINEERED PEPTIDE; CHAIN: E, F;	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE
940	1dh2	A	398	610	2.8e-24	0.05	-0.15		IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A; B; ENGINEERED PEPTIDE; CHAIN: E, F;	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE
940	1dqq	A	128	311	8.4e-26	0.21	-0.07		ANTI-LYSOZYME ANTIBODY HYHEL-63 (LIGHT CHAIN); CHAIN: A, C; ANTI-LYSOZYME ANTIBODY HYHEL-63 (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM ANTI-LYSOZYME ANTIBODY, HYHEL-63, HEN EGG WHITE LYSOZYME
940	1e4k	A	144	303	2.8e-31	0.20	0.46		LOW AFFINITY IMMUNOGLOBULIN	COMPLEX CD16; IGG1-FC COMPLEX, FC FRAGMENT, IGG,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A, B;	FC, RECEPTOR, CD16, GAMMA
940	1e4k	A	221	394	1.1e-37	0.25	-0.11		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A, B;	COMPLEX CD16; IGG1-FC COMPLEX, FC FRAGMENT, IGG, FC, RECEPTOR, CD16, GAMMA
									TAB2; CHAIN: L, M; TAB2; CHAIN: H, I; CYCLIC PEPTIDE; CHAIN: P, Q	COMPLEX (ANTIBODY/ANTIGEN) CROSS-REACTIVITY, PROTEIN-PEPTIDE RECOGNITION
940	1e4x	H	24	224	7e-73	0.22	0.58		TAB2; CHAIN: L, M; TAB2; CHAIN: H, I; CYCLIC PEPTIDE; CHAIN: P, Q	COMPLEX (ANTIBODY/ANTIGEN) CROSS-REACTIVITY, PROTEIN-PEPTIDE RECOGNITION
940	1e4x	H	312	505	4.2e-57	0.29	0.03		TAB2; CHAIN: L, M; TAB2; CHAIN: H, I; CYCLIC PEPTIDE; CHAIN: P, Q	COMPLEX (ANTIBODY/ANTIGEN) CROSS-REACTIVITY, PROTEIN-PEPTIDE RECOGNITION
940	1e5o	H	315	503	2.8e-48	0.25	0.19		IGG2A MONOCLONAL ANTIBODY (LIGHT CHAIN); CHAIN: L; IGG2A MONOCLONAL ANTIBODY (HEAVY CHAIN); CHAIN: H; FMDV PEPTIDE; CHAIN: P;	IMMUNE SYSTEM FMDV, ANTIGENIC-ANTIBODY INTERACTIONS, RGD MOTIF, G-H LOOP 2 OF VP1.
940	1e5t	C	224	395	5.1e-28	0.49	0.68		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFRI; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOLD FOLD
940	1e3d	H	314	505	2.8e-54	0.14	0.03		CATALYTIC ANTIBODY 4B2; CHAIN: L, J; CATALYTIC ANTIBODY	IMMUNE SYSTEM CATALYTIC ANTIBODY, AMIDINIUM, HAPTENCIC CHARGE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
940	1f6a	A	224	399	1.2e-29	0.49	0.72		4B2, CHAIN: H, K; HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D; COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE MONOCLONAL ANTIBODY F9.13.7 (IGG1) 1FBI 3 COMPLEXED WITH LYSOZYME (E.C.3.2.1.17) 1FBI 4	IMMUNE SYSTEM HIGH AFFINITY IGB-FC RECEPTOR, FC(EPSILON) IGB-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
940	1fbi	H	312	502	4.2e-57	0.14	0.33			
940	1fc2	D	144	303	2.8e-31	-0.02	0.46		IMMUNOGLOBULIN IMMUNOGLOBULIN FC AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	
940	1fc2	D	227	394	4.2e-37	0.44	-0.06		IMMUNOGLOBULIN IMMUNOGLOBULIN FC AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	
940	1fc2	D	398	612	4.2e-23	0.10	-0.19		IMMUNOGLOBULIN IMMUNOGLOBULIN FC AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	
940	1fgn	H	25	219	1.3e-66	0.13	0.30		IMMUNOGLOBULIN FAB 5G9, CHAIN: L, H;	IMMUNOGLOBULIN FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN; ANTIBODY, FAB, ANTI-TF, MONOCLONAL, MURINE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
940	1fgn	H	314	500	5.6e-56	0.41	0.00		IMMUNOGLOBULIN FAB 5G9; CHAIN: L, H;	IMMUNOGLOBULIN
940	1fh5	H	318	503	2.8e-47	0.32	0.04		MONOCLONAL ANTIBODY MAK33; CHAIN: L; MONOCLONAL ANTIBODY MAK33; CHAIN: H;	IMMUNE SYSTEM FAB, BIP, CRYSTAL STRUCTURE
940	1fge	L	128	311	2.8e-25	0.31	0.03		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB FRAGMENT 1FIG3	
940	1f3	A	315	501	4.2e-49	0.37	-0.02		BLUE FLUORESCENT ANTIBODY (19G2)-HEAVY CHAIN; CHAIN: H, A; BLUE FLUORESCENT ANTIBODY (19G2)-LIGHT CHAIN; CHAIN: L, B;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
940	1fhs	L	128	311	1.4e-25	0.19	0.03		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A: ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
940	1for	H	314	503	1.4e-53	0.53	-0.06		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB17-1A) (ORTHORHOMBIC	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
940	1f5k	C	312	505	9.8e-58	0.13	0.17		CRYSTAL FORM 1 FOR 3 MAJOR POLLEN ALLERGEN BET V 1-A; CHAIN: A, D, G, J; IMMUNOGLOBULIN KAPPA LIGHT CHAIN; CHAIN: B, E, H, K; ANTIBODY HEAVY CHAIN FAB; CHAIN: C, F, I, L;	IMMUNE SYSTEM BET V 1-A, BETVI ALLERGEN; BV16 FAB-FRAGMENT, KAPPA MOPC21 CODING SEQUENCE; HEAVY CHAIN OF THE MONOCLONAL ANTIBODY MST2; BET V 1, BV16 FAB FRAGMENT, ANTIBODY ALLERGEN COMPLEX
940	1fvd	A	128	311	2.8e-26	0.40	0.48		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
940	1hzh	H	139	499	2.8e-64	0.19	0.35		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K; IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L, M;	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12
940	1hzh	H	229	612	1.4e-29	0.11	-0.03		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K; IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L, M;	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12
940	1hzh	H	24	397	0	0.23	0.25		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K; IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L, M;	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12
940	1hzh	H	312	611	4.2e-61	0.25	0.11		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K;	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L, M;	
940	1ile	A	228	392	4.2e-30	0.31	-0.08		IG GAMMA-2A CHAIN C REGION; CHAIN: A, B;	IMMUNE SYSTEM IGG2A; IGG, FC
940	1ilc	A	399	610	2.8e-20	0.12	-0.17		IG GAMMA-2A CHAIN C REGION; CHAIN: A, B;	IMMUNE SYSTEM IGG2A; IGG, FC
940	1igt	A	128	311	2.8e-25	0.02	0.17		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
940	1igt	B	136	499	1.1e-58	0.04	0.23		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
940	1igt	B	25	393	0	0.35	0.48		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
940	1igt	B	313	611	1.1e-67	0.08	0.03		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
940	1igy	B	136	499	1.4e-58	0.16	0.62		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION, C REGION, HINGE REGION
940	1igy	B	25	392	1.4e-97	0.38	0.10		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION, C REGION, HINGE REGION
940	1igy	B	313	611	5.6e-66	0.12	0.13		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION, C REGION, HINGE REGION
940	1ili	A	314	503	1.3e-53	0.33	0.28		MONOCLONAL ANTIBODY G3-519 (HEAVY CHAIN); CHAIN: A; MONOCLONAL ANTIBODY G3-519 (LIGHT CHAIN); CHAIN:	IMMUNE SYSTEM FAB, BETA SHEET STRUCTURE, ANTIBODY

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
940	1itb	B	230	500	1.4e-36	0.11	0.66		B; INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
940	1kb5	H	25	222	4.2e-70	0.23	0.23		KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
940	1kb5	L	128	311	2.8e-26	0.24	0.43		KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
940	1mam	H	25	220	9.8e-67	-0.01	0.01		IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT (FAB) (GG2B, KAPPA) 1MAM 3	
940	1mco	H	136	499	2.8e-68	0.16	0.66		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (GG1) (MCG) WITH A HINGE DELETION 1MCO 3	
940	1mco	H	227	610	1.4e-32	-0.13	0.13		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (GG1) (MCG) WITH A HINGE DELETION 1MCO	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
940	Imco	H	22	433	0			112.21	3 IMMUNOGLOBULIN G1 (GG1) (MCG) WITH A HINGE DELETION IMCO	
940	Imco	H	24	393	0	0.08	0.89		3 IMMUNOGLOBULIN G1 (GG1) (MCG) WITH A HINGE DELETION IMCO	
940	Imco	H	312	611	4.2e-57	0.31	0.11		3 IMMUNOGLOBULIN G1 (GG1) (MCG) WITH A HINGE DELETION IMCO	
940	Imim	H	314	502	5.6e-48	0.41	0.46		CHIMERIC SDZ CHI621; CHAIN: H, L; IMMUNOGLOBULIN FAB (BV04-01)	IMMUNOGLOBULIN C REGION
940	Inbv	H	25	220	4.2e-66	0.22	-0.12		3 AUTOANTIBODY BINDING SINGLE-STRANDED DNA INBV 3 (UNLIGANDED FORM) INBV 4	
940	Ipig	H	24	220	8.4e-70	0.39	0.17		IGG2A=KAPPA=; 1PLG 4 CHAIN: L, H, 1PLG 5	IMMUNOGLOBULIN
940	Iqfu	H	312	504	2.8e-56	0.36	0.52		HEMAGGLUTININ (HA1 CHAIN); CHAIN: A; HEMAGGLUTININ (HA2 CHAIN); CHAIN: B; IMMUNOGLOBULIN IGG1-KAPPA ANTIBODY (LIGHT CHAIN); CHAIN:	VIRAL PROTEIN/IMMUNE SYSTEM COMPLEX (HEMAGGLUTININ/IMMUNOGLOBULIN), HEMAGGLUTININ, 2 IMMUNOGLOBULIN, VIRAL PROTEIN/IMMUNE SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									L; IMMUNOGLOBULIN IG1-KAPPA ANTIBODY (HEAVY CHAIN); CHAIN: H;	
940	1sm3	H	24	222	1.4e-70	0.09	0.07		SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPTOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPTOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPTOPE)
940	1vge	L	128	311	2.8e-25	0.23	-0.02		TRL9 FAB; CHAIN: L, H;	IMMUNOGLOBULIN TRL9, ANTI-THYROID PEROXIDASE, AUTOANTIBODY, 2 IMMUNOGLOBULIN
940	1wej	H	313	505	1.4e-56	0.32	0.05		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN; IMMUNOGLOBULIN, IG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
940	1wej	L	128	311	1.4e-25	0.19	0.11		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN; IMMUNOGLOBULIN, IG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
940	1wio	A	134	492	8.5e-34	0.13	-0.08		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
940	1w1o	A	319	629	5.1e-18	0.22	-0.17		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	LIPOPROTEIN, POLYMORPHISM
										GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
940	1yej	H	314	502	1.3e-51	0.27	0.03		IG ANTIBODY D2.3 (LIGHT CHAIN); CHAIN: L; IG ANTIBODY D2.3 (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM ABZYME, TRANSITION STATE ANALOG, IMMUNE SYSTEM
940	25c8	H	25	219	1.4e-67	0.28	0.66		IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
940	25c8	H	313	501	1.4e-56	0.26	0.07		IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
940	2cgr	H	25	220	2.8e-66	-0.00	-0.07		IMMUNOGLOBULIN IGG2B (KAPPA) FAB FRAGMENT COMPLEXED WITH ANTIGEN 2CGR 3 N-(P-CYANOPHENYL)-N ¹ -(DIPHENYLEMETHYL) GUANIDINEACETIC ACID 2CGR 4	
940	2fgw	H	25	221	1.4e-69	0.24	0.24		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY Y52' (HUH52-OZ FAB) 2FGW 4	
940	2fgw	L	128	311	7e-27	0.34	0.23		IMMUNOGLOBULIN FAB FRAGMENT OF A	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
941	1a4y	A	7	243	1e-26	0.41	0.96		HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
									RIBONUCLEASE INHIBITOR; CHAIN: A, D, E; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RT-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTIDE MAPPING, LEUCINE-RICH 3 REPEATS
941	1a9n	A	108	242	1e-24	0.73	0.89		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
941	1a9n	A	139	243	7e-07	0.34	1.00		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
941	1a9n	A	25	174	1.2e-21	0.46	0.57		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
941	1a9n	A	48	197	1.5e-25	0.69	0.96		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
941	1a9n	A	66	173	2.8e-06	0.49	0.49		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
941	1a9n	A	90	194	2.8e-06	0.34	0.89		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, C; U2 B"; CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
941	1a9n	C	108	242	6.8e-25	0.73	0.84		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
941	1a9n	C	139	243	7e-07	0.52	1.00		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
941	1a9n	C	30	148	1.7e-18	0.45	0.90		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
941	1a9n	C	48	221	5.1e-26	0.67	0.95		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
941	1d0b	A	156	306	1.4e-18	0.59	0.99		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
941	1d0b	A	23	167	1.4e-23	0.55	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
941	1d0b	A	40	191	8.4e-27	0.56	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
941	1d0b	A	73	239	7e-27	1.21	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
941	1dce	A	163	267	1.4e-10	0.79	0.80		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
941	1dce	A	30	254	1.7e-35	-0.00	-0.05		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
941	1dce	A	90	196	1.4e-11	0.72	0.99		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
941	1ds9	A	23	142	8.4e-13	-0.32	0.19		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
941	1ds9	A	48	237	1.7e-18	-0.21	0.05		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
941	1ds9	A	99	238	2.8e-15	0.01	0.62		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
941	1fo1	A	134	196	1.4e-07	-0.09	0.96		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
941	1fo1	A	182	247	2.8e-07	0.20	0.35		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
941	1fo1	B	134	196	1.4e-07	-0.11	0.89		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
941	1fo1	B	182	247	2.8e-07	0.34	0.42		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
941	1fqv	A	44	240	1.4e-12	0.27	0.37		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
941	1fs2	A	31	240	1e-12	0.38	-0.02		SKP2; CHAIN: A, C, SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
941	1fs2	A	44	241	8.4e-11	0.23	0.27		SKP2; CHAIN: A, C, SKP1; CHAIN: B, D;	ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
941	1fs2	A	88	240	1.4e-12	0.39	0.95		SKP2; CHAIN: A, C, SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
941	1ft8	A	134	196	1.4e-07	-0.03	0.94		TIP ASSOCIATING PROTEIN; CHAIN: A, B, C, D, E;	RNA BINDING PROTEIN TAP; RUBONUCLEOPROTEIN (RNP, RRM, RBD) AND LEUCINE-RICH-REPEAT 2 (LRR) DOMAINS
941	1ft8	A	182	247	2.8e-07	0.76	0.36		TIP ASSOCIATING PROTEIN; CHAIN: A, B, C, D, E;	RNA BINDING PROTEIN TAP; RUBONUCLEOPROTEIN (RNP, RRM, RBD) AND LEUCINE-RICH-REPEAT 2 (LRR) DOMAINS
941	1yfg	A	41	242	1.7e-20	0.42	0.41		GTPASE-ACTIVATING PROTEIN RNAI_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAI; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
941	2bnh		143	335	4.2e-09	0.20	0.11		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RUBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
941	2bnh		30	242	1.7e-24	0.67	0.82		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RUBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
944	1a7c	A	170	532	2.8e-91			151.16	PLASMINOGEN ACTIVATOR INHIBITOR	COMPLEX (PROTEASE INHIBITOR/PEPTIDE) PAI-1;

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									TYPE 1; CHAIN: A; PENTAPEPTIDE; CHAIN: B, C	SERINE PROTEASE INHIBITOR, PAL-1, CARBOHYDRATE, INHIBITOR 2 COMPLEX, PEPTIDE
944	1a7c	A	8	370	2.8e-91			152.25	PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1; CHAIN: A; PENTAPEPTIDE; CHAIN: B, C	COMPLEX (PROTEASE INHIBITOR/PEPTIDE) PAL-1; SERINE PROTEASE INHIBITOR, PAL-1, CARBOHYDRATE, INHIBITOR 2 COMPLEX, PEPTIDE
944	1as4	A	15	337	0			155.82	ANTICHYMOTRYPSIN; CHAIN: A, B;	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR, ANTICHYMOTRYPSIN
944	1as4	A	176	489	4.2e-100	0.32	1.00		ANTICHYMOTRYPSIN; CHAIN: A, B;	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR, ANTICHYMOTRYPSIN
944	1as4	A	177	499	4.2e-100			154.82	ANTICHYMOTRYPSIN; CHAIN: A, B;	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR, ANTICHYMOTRYPSIN
944	1ath	A	163	534	9.8e-98			168.04	HUMAN ANTITHROMBIN-III ANTITHROMBIN III LATH 3	
944	1ath	A	176	532	9.8e-98	0.84	1.00		HUMAN ANTITHROMBIN-III ANTITHROMBIN III LATH 3	
944	1ath	A	1	372	1.4e-97			170.36	HUMAN ANTITHROMBIN-III ANTITHROMBIN III LATH 3	
944	1ath	B	168	533	2.8e-96			137.56	HUMAN ANTITHROMBIN-III ANTITHROMBIN III LATH 3	
944	1ath	B	176	532	2.8e-96	0.70	1.00		HUMAN ANTITHROMBIN-III ANTITHROMBIN III LATH 3	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTITHROMBIN-III ANTITHROMBIN III IATH 3	
944	1ath	B	6	371	8.4e-96			138.93	HUMAN ANTITHROMBIN-III ANTITHROMBIN III IATH 3	
944	1by7	A	10	370	0			148.40	PLASMINOGEN ACTIVATOR INHIBITOR- 2; CHAIN: A;	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING
944	1by7	A	172	532	0			147.26	PLASMINOGEN ACTIVATOR INHIBITOR- 2; CHAIN: A;	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING
944	1by7	A	176	532	0	0.55	1.00		PLASMINOGEN ACTIVATOR INHIBITOR- 2; CHAIN: A;	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING
944	1db2	A	171	532	1.4e-91			162.23	PLASMINOGEN ACTIVATOR INHIBITOR- 1; CHAIN: A, B;	HYDROLASE INHIBITOR NATIVE SERPIN, HYDROLASE INHIBITOR
944	1db2	A	9	370	9.8e-91			163.81	PLASMINOGEN ACTIVATOR INHIBITOR- 1; CHAIN: A, B;	HYDROLASE INHIBITOR NATIVE SERPIN, HYDROLASE INHIBITOR
944	1dzg	I	136	534	2.8e-97			180.38	ANTITHROMBIN-III; CHAIN: I; ANTITHROMBIN-III; CHAIN: I;	SERPIN SERPIN
944	1dzg	I	176	532	2.8e-97	0.48	1.00		ANTITHROMBIN-III; CHAIN: I; ANTITHROMBIN-III; CHAIN: I;	SERPIN SERPIN
944	1dzg	I	1	372	4.2e-97			154.88	ANTITHROMBIN-III; CHAIN: I; ANTITHROMBIN-III; CHAIN: I;	SERPIN SERPIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
944	1ezx	A	12	339	2.8e-98			157.67	ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1-ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1-ANTITRYPSIN, 2 TRYPSIN
944	1ezx	A	174	501	1.4e-99			156.36	ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1-ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1-ANTITRYPSIN, 2 TRYPSIN
944	1ezx	A	175	501	1.4e-99	0.28	1.00		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1-ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1-ANTITRYPSIN, 2 TRYPSIN
944	1f0c	A	185	502	2.8e-66			104.89	ICE INHIBITOR; CHAIN: A; ICE INHIBITOR; CHAIN: B;	VIRUS/VIRAL PROTEIN CYTOKINE RESPONSE MODIFIER PROTEIN, CRMA; CYTOKINE RESPONSE MODIFIER PROTEIN, CRMA; APOPTOSIS, CASPASE INHIBITOR, PROTEASE INHIBITOR, SERPIN
944	1f0c	A	23	340	4.2e-65			106.63	ICE INHIBITOR; CHAIN: A; ICE INHIBITOR; CHAIN: B;	VIRUS/VIRAL PROTEIN CYTOKINE RESPONSE MODIFIER PROTEIN, CRMA; CYTOKINE RESPONSE MODIFIER PROTEIN, CRMA; APOPTOSIS, CASPASE INHIBITOR, SERPIN
944	1hle	A	13	336	4.2e-99			134.44	HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLE) 1HLE 3	
944	1hle	A	175	489	7e-99	0.30	1.00		HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE	